```
!!AA MULTIPLE ALIGNMENT 1.0
PileUp of: us*

Symbol comparison table: GenRunData:blosum62.cmp    CompCheck: 1102

                GapWeight: 8
          GapLengthWeight: 0

pileup.msf  MSF: 1222  Type: P   December 17, 2003 13:31  Check: 3612 ..

 Name: us-09-873-409-3   Len: 1222   Check: 8709   Weight:  1.00
 Name: us-09-873-409-7   Len: 1222   Check: 4278   Weight:  1.00
 Name: us-09-873-409-8   Len: 1222   Check: 9292   Weight:  1.00
 Name: us-09-873-409-1   Len: 1222   Check: 5986   Weight:  1.00
 Name: us-09-873-409-2   Len: 1222   Check: 1428   Weight:  1.00
 Name: us-09-873-409-4   Len: 1222   Check: 4911   Weight:  1.00
 Name: us-09-873-409-5   Len: 1222   Check: 6997   Weight:  1.00
 Name: us-09-873-409-6   Len: 1222   Check: 2011   Weight:  1.00

//


                     1                                                      50
us-09-873-409-3   MILGILASLV  NGACLPLMPL  VLGEMSDNLI  SGCLVQTNTY  SFFRLTLYYV
us-09-873-409-7   MILGILASLV  NGACLPLMPL  VLGEMSDNLI  SGCLVQTNTY  SFFRLTLYYV
us-09-873-409-8   MILGILASLV  NGACLPLMPL  VLGEMSDNLI  SGCLVQTNTY  SFFRLTLYYV
us-09-873-409-1   --------    ----------  ----------  ----------  ----------
us-09-873-409-2   --------    ----------  ----------  ----------  ----------
us-09-873-409-4   --------    ----------  ----------  ----------  ----------
us-09-873-409-5   --------    ----------  ----------  ----------  ----------
us-09-873-409-6   --------    ----------  ----------  ----------  ----------

                     51                                                     100
us-09-873-409-3   GIGVAALIFG  YIQISLWIIT  AARQTKRIRK  QFFHSVLAQD  IGWFDSCDIG
us-09-873-409-7   GIGVAALIFG  YIQISLWIIT  AARQTKRIRK  QFFHSVLAQD  IGWFDSCDIG
us-09-873-409-8   GIGVAALIFG  YIQISLWIIT  AARQTKRIRK  QFFHSVLAQD  IGWFDSCDIG
us-09-873-409-1   --------    ----------  ----------  ----------  ----------
us-09-873-409-2   --------    ----------  ----------  ----------  ----------
us-09-873-409-4   --------    ----------  ----------  ----------  ----------
us-09-873-409-5   --------    ----------  ----------  ----------  ----------
us-09-873-409-6   --------    ----------  ----------  ----------  ----------

                     101                                                    150
us-09-873-409-3   ELNTRMTDID  KISDGIGDKI  ALLFQNMSTP  SIGLAVGLVK  GWKLTLVTLS
us-09-873-409-7   ELNTRMTDID  KISDGIGDKI  ALLFQNMSTP  SIGLAVGLVK  GWKLTLVTLS
us-09-873-409-8   ELNTRMTDID  KISDGIGDKI  ALLFQNMSTP  SIGLAVGLVK  GWKLTLVTLS
us-09-873-409-1   --------    ----------  ----------  ----------  ----------
us-09-873-409-2   --------    ----------  ----------  ----------  ----------
us-09-873-409-4   --------    ----------  ----------  ----------  ----------
us-09-873-409-5   --------    ----------  ----------  ----------  ----------
us-09-873-409-6   --------    ----------  ----------  ----------  ----------

                     151                                                    200
us-09-873-409-3   TSPLIMASAA  ACSRMVISLT  SKELSAYSKA  GAVAEEVLSS  IRTVIAFRAQ
us-09-873-409-7   TSPLIMASAA  ACSRMVISLT  SKELSAYSKA  GAVAEEVLSS  IRTVIAFRAQ
us-09-873-409-8   TSPLIMASAA  ACSRMVISLT  SKELSAYSKA  GAVAEEVLSS  IRTVIAFRAQ
us-09-873-409-1   --------    ----------  ----------  ----------  ----------
us-09-873-409-2   --------    --MVISLT    SKELSAYSKA  GAVAEEVLSS  IRTVIAFRAQ
us-09-873-409-4   --------    ----------  ----------  ----------  ----------
us-09-873-409-5   --------    ----------  ----------  ----------  ----------
us-09-873-409-6   --------    ----------  ----------  ----------  ----------

                     201                                                    250
us-09-873-409-3   EKELQRSFLL  NITRYAWPYP  POWLLSCVLX  FVRYTQNLKD  AKDFGIKRTI
us-09-873-409-7   EKELQRSFLL  NITRYAWPYP  POWLLSCVLX  FVRYTQNLKD  AKDFGIKRTI
us-09-873-409-8   EKELQ....   .........   .RYTQNLKD   AKDFGIKRTI
us-09-873-409-1   EKELQ....   .........   .RYTQNLKD   AKDFGIKRTI
us-09-873-409-2   EKELQRSFLL  NITRYAWPYP  POWLLSCVLX  FVRYTQNLKD  AKDFGIKRTI
us-09-873-409-4   EKELQRSFLL  NITRYAWPYP  POWLLSCVLX  FVRYTQNLKD  AKDFGIKRTI
us-09-873-409-5   EKELQRSFLL  NITRYAWPYP  POWLLSCVLX  FVRYTQNLKD  AKDFGIKRTI
us-09-873-409-6   EKELQ....   .........   .RYTQNLKD   AKDFGIKRTI

                     251                                                    300
us-09-873-409-3   --------    ----------  ----------  ----------  ----------
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                     301                                                    350
us-09-873-409-7   ASKVSLGAVY  FFMNGTYGLA  FWYGTSLLIN  GBPGYTIGTV  LAVFFSVIHS
us-09-873-409-8   ASKVSLGAVY  FFMNGTYGLA  FWYGTSLLIN  GBPGYTIGTV  LAVFFSVIHS
us-09-873-409-1   ASKVSLGAVY  FFMNGTYGLA  FWYGTSLLIN  GBPGYTIGTV  LAVFFSVIHS
us-09-873-409-2   ASKVSLGAVY  FFMNGTYGLA  FWYGTSLLIN  GBPGYTIGTV  LAVFFSVIHS
us-09-873-409-4   ASKVSLGAVY  FFMNGTYGLA  FWYGTSLLIN  GBPGYTIGTV  LAVFFSVIHS
us-09-873-409-5   ASKVSLGAVY  FFMNGTYGLA  FWYGTSLLIN  GBPGYTIGTV  LAVFFSVIHS
us-09-873-409-6   ASKVSLGAVY  FFMNGTYGLA  FWYGTSLLIN  GBPGYTIGTV  LAVFFSVIHS

                     351                                                    400
us-09-873-409-3   SYCIGRAAVPH  FETFAIARGA  AFHIFQVIDK  KPSIDNFSTA  GYKPESIEGT
us-09-873-409-7   VEPKNVSFNY   PSRPSIKILK  GLNLRIKSGB  TVALVGLNGS  GKSTVVQLLQ
us-09-873-409-8   VEPKNVSFNY   PSRPSIKILK  GLNLRIKSGB  TVALVGLNGS  GKSTVVQLLQ
us-09-873-409-1   SYCIGRAAVPH  FETFAIARGA  AFHIFQVIDK  KPSIDNFSTA  GYKPESIEGT
us-09-873-409-2   SYCIGRAAVPH  FETFAIARGA  AFHIFQVIDK  KPSIDNFSTA  GYKPESIEGT
us-09-873-409-4   VEPKNVSFNY   PSRPSIKILK  GLNLRIKSGB  TVALVGLNGS  GKSTVVQLLQ
us-09-873-409-5   VEPKNVSFNY   PSRPSIKILK  GLNLRIKSGB  TVALVGLNGS  GKSTVVQLLQ
us-09-873-409-6   SYCIGRAAVPH  FETFAIARGA  AFHIFQVIDK  KPSIDNFSTA  GYKPESIEGT

                     401                                                    450
us-09-873-409-3   MVDENDIRAL  NVRHYRDHIG  VVSQBPVLFG  TTISNNIKYG
us-09-873-409-7   RLYDPDDGPI  MVDENDIRAL  NVRHYRDHIG  VVSQBPVLFG  TTISNNIKYG
us-09-873-409-8   RLYDPDDGPI  MVDENDIRAL  NVRHYRDHIG  VVSQBPVLFG  TTISNNIKYG
us-09-873-409-1   RLYDPDDGFI  MVDENDIRAL  NVRHYRDHIG  VVSQBPVLFG  TTISNNIKYG
us-09-873-409-2   MVDENDIRAL  NVRHYRDHIG  VVSQBPVLFG  TTISNNIKYG
us-09-873-409-4   RLYDPDDGFI  MVDENDIRAL  NVRHYRDHIG  VVSQBPVLFG  TTISNNIKYG
us-09-873-409-5   RLYDPDDGFI  MVDENDIRAL  NVRHYRDHIG  VVSQBPVLFG  TTISNNIKYG
us-09-873-409-6   RLYDPDDGFI  MVDENDIRAL  NVRHYRDHIG  VVSQBPVLFG  TTISNNIKYG

                     451                                                    500
us-09-873-409-3   RDDVTDBEME  RAARBANAYD  FIMEFPNKFN  TLVGEKGAQM  SGGQKQRIAI
us-09-873-409-7   RDDVTDBEME  RAARBANAYD  FIMEFPNKFN  TLVGEKGAQM  SGGQKQRIAI
us-09-873-409-8   RDDVTDBEME  RAARBANAYD  FIMEFPNKFN  TLVGEKGAQM  SGGQKQRIAI
us-09-873-409-1   RDDVTDBEME  RAARBANAYD  FIMEFPNKFN  TLVGEKGAQM  SGGQKQRIAI
us-09-873-409-2   RDDVTDBEME  RAARBANAYD  FIMEFPNKFN  TLVGEKGAQM  SGGQKQRIAI
us-09-873-409-4   RDDVTDBEME  RAARBANAYD  FIMEFPNKFN  TLVGEKGAQM  SGGQKQRIAI
us-09-873-409-5   RDDVTDBEME  RAARBANAYD  FIMEFPNKFN  TLVGEKGAQM  SGGQKQRIAI
us-09-873-409-6   RDDVTDBEME  RAARBANAYD  FIMEFPNKFN  TLVGEKGAQM  SGGQKQRIAI

                     501                                                    550
us-09-873-409-3   ARALVRNPKI  LILDEATSAL  DSESKSAVQA  ALEKDT.....
us-09-873-409-7   ARALVRNPKI  LILDEATSAL  DSESKSAVQA  ALEKDT.....
us-09-873-409-8   ARALVRNPKI  LILDEATSAL  DSESKSAVQA  ALEKDT.....
us-09-873-409-1   ARALVRNPKI  LILDEATSAL  DSESKSAVQA  ALEKASKGRT  TIVVAHRLST
us-09-873-409-2   ARALVRNPKI  LILDEATSAL  DSESKSAVQA  ALEKASKGRT  TIVVAHRLST
us-09-873-409-4   ARALVRNPKI  LILDEATSAL  DSESKSAVQA  ALEKASKGRT  TIVVAHRLST
us-09-873-409-5   ARALVRNPKI  LILDEATSAL  DSESKSAVQA  ALEKASKGRT  TIVVAHRLST
us-09-873-409-6   ARALVRNPKI  LILDEATSAL  DSESKSAVQA  ALEKASKGRT  TIVVAHRLST

                     551                                                    600
us-09-873-409-3   .........   .........   .........   .........   .........
us-09-873-409-1   IRSADLIVTL  KDGMLABKGA  HAELMAKRGL  YSSLVMSQDI  KRADBQMBSM
us-09-873-409-2   --MLABKGA   IRSADLIVTL  KDGMLABKGA  HAELMAKRGL  YSSLVMSQDI  KRADBQMBSM
us-09-873-409-4   IRSADLIVTL  KDGMLABKGA  HAELMAKRGL  YSSLVMSQDI  KRADBQMBSM
us-09-873-409-5   IRSADLIVTL  KDGMLABKGA  HAELMAKRGL  YSSLVMSQDI  KRADBQMBSM
us-09-873-409-6   IRSADLIVTL  KDGMLABKGA  HAELMAKRGL  YSSLVMSQDI  KRADBQMBSM

                     601                                                    650
us-09-873-409-3   .........   .........   .........   .........   .........
us-09-873-409-8   .........   .........   .........   .........   .........
us-09-873-409-1   TYSTERKTNS  LPLHSVKSIK  SDFIDKAEES  TQSKBISLPB  VSLLKILKLN
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us-09-873-409-2  TYSTERKTNS LPLHSVKSIK SDFIDKAEES TQSKEISLPE VSLLKILKLN
us-09-873-409-7  TYSTERKTNS LPLHSVKSIK SDFIDKAEES TQSKEISLPE VSLLKILKLN
us-09-873-409-4  TYSTERKTNS LPLHSVKSIK SDFIDKAEES TQSKEISLPE VSLLKILKLN
us-09-873-409-5  TYSTERKTNS LPLHSVKSIK SDFIDKAEES TQSKEISLPE VSLLKILKLN
us-09-873-409-6  TYSTERKTNS LPLHSVKSIK SDFIDKAEES TQSKEISLPE VSLLKILKLN

651                                                                  700
us-09-873-409-3  KPEWPFVVLG TLASVLNGTV HPVFSIIFAK IITMFGNNDK TTLKHDAEIY
us-09-873-409-8  KPEWPFVVLG TLASVLNGTV HPVFSIIFAK IITMFGNNDK TTLKHDAEIY
us-09-873-409-7  KPEWPFVVLG TLASVLNGTV HPVFSIIFAK IITMFGNNDK TTLKHDAEIY
us-09-873-409-1  KPEWPFVVLG TLASVLNGTV HPVFSIIFAK IITMFGNNDK TTLKHDAEIY
us-09-873-409-2  KPEWPFVVLG TLASVLNGTV HPVFSIIFAK IITMFGNNDK TTLKHDAEIY
us-09-873-409-4  KPEWPFVVLG TLASVLNGTV HPVFSIIFAK IITMFGNNDK TTLKHDAEIY
us-09-873-409-5  KPEWPFVVLG TLASVLNGTV HPVFSIIFAK IITMFGNNDK TTLKHDAEIY
us-09-873-409-6  SMIFVILGVI CFVSYPMQGL FYGRAGEILT MRLRHLAFKA MLYQDIAWFD

701                                                                  750
us-09-873-409-3  SMIFVILGVI CFVSYPMQGL FYGRAGEILT MRLRHLAFKA MLYQDIAWFD
us-09-873-409-8  SMIFVILGVI CFVSYPMQGL FYGRAGEILT MRLRHLAFKA MLYQDIAWFD
us-09-873-409-7  SMIFVILGVI CFVSYPMQGL FYGRAGEILT MRLRHLAFKA MLYQDIAWFD
us-09-873-409-1  SMIFVILGVI CFVSYPMQGL FYGRAGEILT MRLRHLAFKA MLYQDIAWFD
us-09-873-409-2  SMIFVILGVI CFVSYPMQGL FYGRAGEILT MRLRHLAFKA MLYQDIAWFD
us-09-873-409-4  SMIFVILGVI CFVSYPMQGL FYGRAGEILT MRLRHLAFKA MLYQDIAWFD
us-09-873-409-5  SMIFVILGVI CFVSYPMQGL FYGRAGEILT MRLRHLAFKA MLYQDIAWFD
us-09-873-409-6  EKENSTGGLT TILAIDIAQI QGATGSRIGV LTQNATNNGL SVIISFIYGW

751                                                                  800
us-09-873-409-3  EKENSTGGLT TILAIDIAQI QGATGSRIGV LTQNATNNGL SVIISFIYGW
us-09-873-409-8  EKENSTGGLT TILAIDIAQI QGATGSRIGV LTQNATNNGL SVIISFIYGW
us-09-873-409-7  EKENSTGGLT TILAIDIAQI QGATGSRIGV LTQNATNNGL SVIISFIYGW
us-09-873-409-1  EKENSTGGLT TILAIDIAQI QGATGSRIGV LTQNATNNGL SVIISFIYGW
us-09-873-409-2  EKENSTGGLT TILAIDIAQI QGATGSRIGV LTQNATNNGL SVIISFIYGW
us-09-873-409-4  EKENSTGGLT TILAIDIAQI QGATGSRIGV LTQNATNNGL SVIISFIYGW
us-09-873-409-5  EKENSTGGLT TILAIDIAQI QGATGSRIGV LTQNATNNGL SVIISFIYGW
us-09-873-409-6  EMTFLILSIA PVLAVTGMIE TAAMTGPANK DKQELKHAGK IATEALENIR

801                                                                  850
us-09-873-409-3  EMTFLILSIA PVLAVTGMIE TAAMTGPANK DKQELKHAGK IATEALENIR
us-09-873-409-8  EMTFLILSIA PVLAVTGMIE TAAMTGPANK DKQELKHAGK IATEALENIR
us-09-873-409-7  EMTFLILSIA PVLAVTGMIE TAAMTGPANK DKQELKHAGK IATEALENIR
us-09-873-409-1  EMTFLILSIA PVLAVTGMIE TAAMTGPANK DKQELKHAGK IATEALENIR
us-09-873-409-2  EMTFLILSIA PVLAVTGMIE TAAMTGPANK DKQELKHAGK IATEALENIR
us-09-873-409-4  EMTFLILSIA PVLAVTGMIE TAAMTGPANK DKQELKHAGK IATEALENIR
us-09-873-409-5  EMTFLILSIA PVLAVTGMIE TAAMTGPANK DKQELKHAGK IATEALENIR
us-09-873-409-6  TIVSLTREKA FEQMYEEMLQ TQHRNTSKKA QIIGSCYAFS HAFIYFAVAA

851                                                                  900
us-09-873-409-3  TIVSLTREKA FEQMYEEMLQ TQHRNTSKKA QIIGSCYAFS HAFIYFAVAA
us-09-873-409-8  TIVSLTREKA FEQMYEEMLQ TQHRNTSKKA QIIGSCYAFS HAFIYFAVAA
us-09-873-409-7  TIVSLTREKA FEQMYEEMLQ TQHRNTSKKA QIIGSCYAFS HAFIYFAVAA
us-09-873-409-1  TIVSLTREKA FEQMYEEMLQ TQHRNTSKKA QIIGSCYAFS HAFIYFAVAA
us-09-873-409-2  TIVSLTREKA FEQMYEEMLQ TQHRNTSKKA QIIGSCYAFS HAFIYFAVAA
us-09-873-409-4  TIVSLTREKA FEQMYEEMLQ TQHRNTSKKA QIIGSCYAFS HAFIYFAVAA
us-09-873-409-5  TIVSLTREKA FEQMYEEMLQ TQHRNTSKKA QIIGSCYAFS HAFIYFAVAA
us-09-873-409-6  GFRFGAYLIQ AGRMTPEGMF IVFTAIAYGA MAIGKTLVLA PEYSKAKSGA

901                                                                  950
us-09-873-409-3  GFRFGAYLIQ AGRMTPEGMF IVFTAIAYGA MAIGKTLVLA PEYSKAKSGA
us-09-873-409-8  GFRFGAYLIQ AGRMTPEGMF IVFTAIAYGA MAIGKTLVLA PEYSKAKSGA
us-09-873-409-7  GFRFGAYLIQ AGRMTPEGMF IVFTAIAYGA MAIGKTLVLA PEYSKAKSGA
us-09-873-409-1  GFRFGAYLIQ AGRMTPEGMF IVFTAIAYGA MAIGKTLVLA PEYSKAKSGA
us-09-873-409-2  GFRFGAYLIQ AGRMTPEGMF IVFTAIAYGA MAIGKTLVLA PEYSKAKSGA
us-09-873-409-4  GFRFGAYLIQ AGRMTPEGMF IVFTAIAYGA MAIGKTLVLA PEYSKAKSGA
us-09-873-409-5  GFRFGAYLIQ AGRMTPEGMF IVFTAIAYGA MAIGKTLVLA PEYSKAKSGA
us-09-873-409-6  AHLFALLEKK PNIDSRSQEG KKPDTCEGNL EFREVSFPYP CRPDVFILRG

951                                                                  1000
us-09-873-409-3  AHLFALLEKK PNIDSRSQEG KKPDTCEGNL EFREVSFPYP CRPDVFILRG
us-09-873-409-8  AHLFALLEKK PNIDSRSQEG KKPDTCEGNL EFREVSFPYP CRPDVFILRG
us-09-873-409-7  AHLFALLEKK PNIDSRSQEG KKPDTCEGNL EFREVSFPYP CRPDVFILRG
us-09-873-409-1  AHLFALLEKK PNIDSRSQEG KKPDTCEGNL EFREVSFPYP CRPDVFILRG
us-09-873-409-2  AHLFALLEKK PNIDSRSQEG KKPDTCEGNL EFREVSFPYP CRPDVFILRG
us-09-873-409-4  AHLFALLEKK PNIDSRSQEG KKPDTCEGNL EFREVSFPYP CRPDVFILRG
us-09-873-409-5  AHLFALLEKK PNIDSRSQEG KKPDTCEGNL EFREVSFPYP CRPDVFILRG
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us-09-873-409-6  AHLFALLEKK PNIDSRSQEG KKPDTCEGNL EFREVSFPYP CRPDVFILRG

1001                                                                 1050
us-09-873-409-3  LSLSIERGKT VAFVGSSGCG KSTSVQLLQR LYDPVQGQVL FDGVDAKELN
us-09-873-409-8  .......... .......... .......... .......... ..........
us-09-873-409-7  .......... .......... .......... .......... ..........
us-09-873-409-1  LSLSIERGKT VAFVGSSGCG KSTSVQLLQR LYDPVQGQVL FDGVDAKELN
us-09-873-409-2  LSLSIERGKT VAFVGSSGCG KSTSVQLLQR LYDPVQGQVL FDGVDAKELN
us-09-873-409-4  LSLSIERGKT VAFVGSSGCG KSTSVQLLQR LYDPVQGQVL FDGVDAKELN
us-09-873-409-5  LSLSIERGKT VAFVGSSGCG KSTSVQLLQR LYDPVQGQVL FDGVDAKELN
us-09-873-409-6  VQWLRSQIAI VPQEPVLFNC SIAENIAYGD NSRVVPLDEI KEAANAANIH

1051                                                                 1100
us-09-873-409-3  VQWLRSQIAI VPQEPVLFNC SIAENIAYGD NSRVVPLDEI KEAANAANIH
us-09-873-409-8  .......... .......... .......... .......... ..........
us-09-873-409-7  .......... .......... .......... .......... ..........
us-09-873-409-1  VQWLRSQIAI VPQEPVLFNC SIAENIAYGD NSRVVPLDEI KEAANAANIH
us-09-873-409-2  VQWLRSQIAI VPQEPVLFNC SIAENIAYGD NSRVVPLDEI KEAANAANIH
us-09-873-409-4  VQWLRSQIAI VPQEPVLFNC SIAENIAYGD NSRVVPLDEI KEAANAANIH
us-09-873-409-5  VQWLRSQIAI VPQEPVLFNC SIAENIAYGD NSRVVPLDEI KEAANAANIH
us-09-873-409-6  SFIEGLPEKY NTQVGLKGAQ LSGGQKQRLA IARALLQKPK ILLLDEATSA

1101                                                                 1150
us-09-873-409-3  SFIEGLPEKY NTQVGLKGAQ LSGGQKQRLA IARALLQKPK ILLLDEATSA
us-09-873-409-8  .......... .......... .......... .......... ..........
us-09-873-409-7  .......... .......... .......... .......... ..........
us-09-873-409-1  SFIEGLPEKY NTQVGLKGAQ LSGGQKQRLA IARALLQKPK ILLLDEATSA
us-09-873-409-2  SFIEGLPEKY NTQVGLKGAQ LSGGQKQRLA IARALLQKPK ILLLDEATSA
us-09-873-409-4  SFIEGLPEKY NTQVGLKGAQ LSGGQKQRLA IARALLQKPK ILLLDEATSA.
us-09-873-409-5  SFIEGLPEKY NTQVGLKGAQ LSGGQKQRLA IARALLQKPK ILLLDEATSA
us-09-873-409-6  LDNDSEKVVQ HALDKARTGR TCLVVTHRLS AIQNADLIVV LHNGKIKEQG

1151                                                                 1200
us-09-873-409-3  LDNDSEKVVQ HALDKARTGR TCLVVTHRLS AIQNADLIVV LHNGKIKEQG
us-09-873-409-8  .......... .......... .......... .......... ..........
us-09-873-409-7  .......... .......... .......... .......... ..........
us-09-873-409-1  LDNDSEKVVQ HALDKARTGR TCLVVTHRLS AIQNADLIVV LHNGKIKEQG
us-09-873-409-2  LDNDSEKVVQ HALDKARTGR TCLVVTHRLS AIQNADLIVV LHNGKIKEQG
us-09-873-409-4  LDNDSEKVVQ HALDKARTGR TCLVVTHRLS AIQNADLIVV LHNGKIKEQG
us-09-873-409-5  LDNDSEKVVQ HALDKARTGR TCLVVTHRLS AIQNADLIVV LHNGKIKEQG
us-09-873-409-6  THQELLRNRD IYFKLVNAQS VQ

1201                                                    1222
us-09-873-409-3  THQELLRNRD IYFKLVNAQS VQ
us-09-873-409-8  .......... F--------- --
us-09-873-409-7  .......... F--------- --
us-09-873-409-1  THQELLRNRD IYFKLVNAQS VQ
us-09-873-409-2  THQELLRNRD IYFKLVNAQS VQ
us-09-873-409-4  THQELLRNRD IYFKLVNAQS VQ
us-09-873-409-5  THQELLRNRD IYFKLVNAQS VQ
us-09-873-409-6  THQELLRNRD IYFKLVNAQS VQ
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!!AA_MULTIPLE_ALIGNMENT 1.0
PileUp of: us*

Symbol comparison table: GenRunData:blosum62.cmp  CompCheck: 1102

        GapWeight: 8
        GapLengthWeight: 0

pileup2.msf  MSF: 1222  Type: P  December 17, 2003 13:38  Check: 8425 ..

Name: us-09-873-409-2  Len:  1222  Check: 1428  Weight:  1.00
Name: us-09-873-409-5  Len:  1222  Check: 6997  Weight:  1.00

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                              1
us-09-873-409-2 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~    50
us-09-873-409-5 MILGILASLV NGACLPLMPL VLGEMSDNLI SGCLVQTNTY SFFRLTLYYV    50

                             51
us-09-873-409-2 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~   100
us-09-873-409-5 GIGVAALIFG YIQISLWIIT AARQTKRIRK QFFHSVLAQD IGWFDSCDIG   100

                            101
us-09-873-409-2 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~   150
us-09-873-409-5 ELNTRMTDID KISDGIGDKI ALLFQNMSTF SIGLAVGLVK GWKILTVTLS   150

                            151
us-09-873-409-2 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~   200
us-09-873-409-5 TSPLIMASAA ACSRMVISLT SKELSAYSKA GAVAEEVLSS IRTVIAFRAQ   200

                            201
us-09-873-409-2 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~   250
us-09-873-409-5 EKELQRSFLL NITRYAWFYF PQWLLSCVLK FVRYTQNLKD AKDFGIKRTI   250

                            251
us-09-873-409-2 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~   300
us-09-873-409-5 ASKVSLGAVY FFMNGTYGLA FWYGTSLLIN GEPGYITGTV LAVFPSVIHS   300

                            301
us-09-873-409-2 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~   350
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                            351
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us-09-873-409-5 RLYDPDDGPI MVDENDIRAL NVRHYRDHIG VVSQEPVLFG TTISNNIKYG   450

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us-09-873-409-5 RDDVTDEEME RAAREANAYD PIMEFPNKFN TLVGEKGAQM SGGQKQRIAI   500

                            501
us-09-873-409-2 ARALVRNPKI LILDEATSAL DSESKSAVQA ALEKASKGRT TIVVAHRLST   550
us-09-873-409-5 ARALVRNPKI LILDEATSAL DSESKSAVQA ALEKASKGRT TIVVAHRLST   550

                            551
us-09-873-409-2 IRSADLIVTL KDGMLAEKGA HAELMAKRGL YYSLVMSQDI KKADEQMESM   600
us-09-873-409-5 IRSADLIVTL KDGMLAEKGA HAELMAKRGL YYSLVMSQDI KKADEQMESM   600

                            601
us-09-873-409-2 TYSTERKTNS LPLHSVKSIK SDFIDKAEES TQSKEISLPE VSLLKIKLN    650
us-09-873-409-5 TYSTERKTNS LPLHSVKSIK SDFIDKAEES TQSKEISLPE VSLLKIKLN    650

                            651
us-09-873-409-2 KPEWPFVVLG TLASVLNGTV HPVFSIIFAK IITMFGNNDK TTLKHDAEIY   700
us-09-873-409-5 KPEWPFVVLG TLASVLNGTV HPVFSIIFAK IITMFGNNDK TTLKHDAEIY   700

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us-09-873-409-5 SMIFVILGVI CFVSYFMQGL FYGRAGEILT MRLRHLAFKA MLYQDIAWFD   750

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us-09-873-409-5 EKENSTGGLT TILAIDIAQI QGATGSRIGV LTQNATNMGL SVIISPIYGW   800

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us-09-873-409-5 EMTFLILSIA PVLAVTGMIE TAAMTGFANK DKQELKHAGK IATEALENIR   850

                            851
us-09-873-409-2 TIVSLTREKA FEQMYEBMLQ TQHRNTSKRA QIIGSCYAPS HAFIYFAVAA   900
us-09-873-409-5 TIVSLTREKA FEQMYEBMLQ TQHRNTSKRA QIIGSCYAPS HAFIYFAVAA   900

                            901
us-09-873-409-2 GFRFGAYLIQ AGRMTPEGMF IVFTAIAYGA MAIGKTLVLA PEYSKAKSGA   950
us-09-873-409-5 GFRFGAYLIQ AGRMTPEGMF IVFTAIAYGA MAIGKTLVLA PEYSKAKSGA   950

                            951
us-09-873-409-2 AHLFALLEKK PNIDSRSQBG KKPDTCBGNL BFRBVSFPYP CRPDVFILRG  1000
us-09-873-409-5 AHLFALLEKK PNIDSRSQBG KKPDTCBGNL BFRBVSFPYP CRPDVFILRG  1000

                           1001
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us-09-873-409-5 VQWLRSQIAI VPQBPVLFNC SIAENIAYGD NSRVVPLDEI KRAANAANIH  1100

                           1101
us-09-873-409-2 SFIBGLPEKY NTQVGLKGAQ LSGGQKQRIA IARALLQKPK ILLLDEATSA  1150
us-09-873-409-5 SFIBGLPEKY NTQVGLKGAQ LSGGQKQRIA IARALLQKPK ILLLDEATSA  1150

                           1151
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us-09-873-409-5 LDNDSEKVVQ HALDKARTGR TCLVVTHRLS AIQNADLIVV LHNGKIKEQG  1200

                           1201
us-09-873-409-2 THQBLLRNRD IYFKLVNAQS VQ                               1222
us-09-873-409-5 THQBLLRNRD IYFKLVNAQS VQ                               1222
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GAP of: us-09-873-409-2 check: 7710 from: 1 to: 812
PROMIG of: /staff_overflow/sdavid-tmp/dectemp/yu409/US09873409.pep
sequence 2, application us/09873409
general information:
applicant: frank, markus
applicant: sayegh, mohamed
title of invention: a gene encoding a multidrug resistance human
p-glycoprotein

to: us-09-873-409-5 check: 6997 from: 1 to: 1222
PROMIG of: /staff_overflow/sdavid-tmp/dectemp/yu409/US09873409.pep
sequence 5, application us/09873409
general information:
applicant: frank, markus
applicant: sayegh, mohamed
title of invention: a gene encoding a multidrug resistance human
p-glycoprotein

Symbol comparison table: /SIDS/appl/gcg/gcgcore/data/rundata/blosum62.cmp
CompCheck: 1102

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        Gap Weight:     8      Average Match:    2.778
     Length Weight:     0      Average Mismatch: -2.248

           Quality:  4079          Length:       1222
             Ratio:  5.023           Gaps:          0
Percent Similarity: 100.000  Percent Identity: 100.000
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Match display thresholds for the alignment(s):
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        | = IDENTITY
        : = 2
        . = 1
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us-09-873-409-2 x us-09-873-409-5 December 17, 2003 13:39

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   1 ...........MVDENDIRALNVRHYRDHIGVVSQEPVLFGTTISNNIKYG  40
                 |||||||||||||||||||||||||||||||||||||||
 401 RLYDPDDGPIMVDENDIRALNVRHYRDHIGVVSQEPVLFGTTISNNIKYG 450

  41 RDDVTDEEMERARREANAYDPIMEFPNKPNTLVGEKGAQMSGGQKQRIAI  90
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 451 RDDVTDEEMERARREANAYDPIMEFPNKPNTLVGEKGAQMSGGQKQRIAI 500

  91 ARALVRNPKILLLDEATSALDSESKSAVQAALEKASKGRTTIVVAHRLST 140
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 501 ARALVRNPKILLLDEATSALDSESKSAVQAALEKASKGRTTIVVAHRLST 550

 141 IRSADLIVTLKDGMLAEKGAHAELMAKRGLYYSLVMSQDIKKADBQMESM 190
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 551 IRSADLIVTLKDGMLAEKGAHAELMAKRGLYYSLVMSQDIKKADBQMESM 600

 191 TYSTERKTNSLPLHSVKSIKSDFIDKAEESTQSKEISLPEVSLLKILKLN 240
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 601 TYSTERKTNSLPLHSVKSIKSDFIDKAEESTQSKEISLPEVSLLKILKLN 650

 241 KPEWPFVVLGTLASVLNGTVHPVFSIIFAKIITMFGNNDKTTLKHDAEIY 290
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 651 KPEWPFVVLGTLASVLNGTVHPVFSIIFAKIITMFGNNDKTTLKHDAEIY 700

 291 SMIFVILGVICFVSYFMQGLFYGRAGEILTMRLRHLAFRAMLYQDIAWFD 340
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 701 SMIFVILGVICFVSYFMQGLFYGRAGEILTMRLRHLAFRAMLYQDIAWFD 750

 341 EKENSTGGLITTILAIDIAQIQGATGSRIGVLTQNATNMGLSVIISPIYGW 390
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 751 EKENSTGGLITTILAIDIAQIQGATGSRIGVLTQNATNMGLSVIISPIYGW 800

 391 EMTFLILSIAPVLAVTGMIETAAMTGFANKDKQELKHAGKIATEALENIR 440
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 801 EMTFLILSIAPVLAVTGMIETAAMTGFANKDKQELKHAGKIATEALENIR 850

 441 TIVSLTREKAFEQMYEEMLQTQHRNTSKKAQIIGSSYAFSHAFIYFAYAA 490
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 851 TIVSLTREKAFEQMYEEMLQTQHRNTSKKAQIIGSSYAFSHAFIYFAYAA 900

 491 GFRPGAYLIQAGRMTPEGMPIVFTAIAYGAMAIGKTLVLAPEYSKAKSGA 540
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 901 GFRPGAYLIQAGRMTPEGMPIVFTAIAYGAMAIGKTLVLAPEYSKAKSGA 950

 541 AHLFALLEKPNIDSRSQEGKKPDTCEGNLEFREVSFFYPCRPDVPILRG 590
     ||||||||||||||||||||||||||||||||||||||||||||||||
 951 AHLFALLEKPNIDSRSQEGKKPDTCEGNLEFREVSFFYPCRPDVPILRG 1000

 591 LSLSIERGKTVAFVGSSSGCGKSTSVQLLQRLYDPVQGQVLFDGVDAKELN 640
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1001 LSLSIERGKTVAFVGSSSGCGKSTSVQLLQRLYDPVQGQVLFDGVDAKELN 1050

 641 VQWLRSQIAIVPQEPVLFNCSIAENIAYGDNSRVVPLDEIKEAANANIH 690
     ||||||||||||||||||||||||||||||||||||||||||||||||
1051 VQWLRSQIAIVPQEPVLFNCSIAENIAYGDNSRVVPLDEIKEAANANIH 1100

 691 SFIEGLPEKYNTQVGLKGAQLSGGQKQRLAIARALLQKPKILLLDEATSA 740
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1101 SFIEGLPEKYNTQVGLKGAQLSGGQKQRLAIARALLQKPKILLLDEATSA 1150

 741 LDNDSEKVVQHALDKARTGRTCLVVTHRLSAIQNADLIVVLHNGKIKEQG 790
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1151 LDNDSEKVVQHALDKARTGRTCLVVTHRLSAIQNADLIVVLHNGKIKEQG 1200

 791 THQELLRNRDIYFKLVNAQSVQ 812
     ||||||||||||||||||||||
1201 THQELLRNRDIYFKLVNAQSVQ 1222
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OM protein - nucleic search, using frame_plus_p2n model

```
                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2003 Compugen Ltd.
```

Run on: December 17, 2003, 14:41:08 ; Search time 83 Seconds
                    (without alignments)
                    2.344 Million cell updates/sec

Title:
Perfect score: 6159
Sequence: u8-09-873-409-5
           1 MILGIIASLVNGACLPLMPL..............QELLRNRDIYFKLVNAQSVQ 1222

Scoring table:
                    BLOSUM62
           Xgapop 10.0 ; Xgapext 0.5
           Ygapop 10.0 ; Ygapext 0.5
           Fgapop   6.0 ; Fgapext 7.0
           Delop   6.0 ; Delext   7.0

Searched: 1 seqs, 79611 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 listing first 1 summaries

Command line parameters:
-MODEL=frame+_p2n.model
-SUFFIX=pto -OUT=aligns1997 -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits
-START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cd1 -LIST=1 -DCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO_XLPXY
-NEG_SCORES=0 -LONGLOG -THREADS=0 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   2341014_1997;*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	932	15.1	79611	1	AC002486	ACCESSION:AC002486

ALIGNMENTS

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AC002486      79611 bp    DNA       linear   PRI 22-AUG-1997
Human BAC clone RG367O17 from 7p15-p21, complete sequence.
```

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LOCUS       AC002486    79611 bp    DNA    linear   PRI 22-AUG-1997
DEFINITION  Human BAC clone RG367O17 from 7p15-p21, complete sequence.
ACCESSION   AC002486
VERSION     AC002486.1  GI:2341014
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 79611)
  AUTHORS   Kalicki,J., Smith,A. and Gibson,A.
  TITLE     The sequence of H. sapiens BAC clone RG367O17
  JOURNAL   Unpublished (1997)
REFERENCE   2  (bases 1 to 79611)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-AUG-1997) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     SUBMITTED BY:
            Genome Sequencing Center
            Department of Genetics
            Washington University
            St. Louis MO 63108, USA
            http://genome.wustl.edu/gsc
            mailto:sapiens@watson.wustl.edu

            NOTICE: This sequence may not represent the entire insert of this
            clone. It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded or sequenced with an alternate
            chemistry; an attempt was made to resolve all sequencing problems,
            such as compressions and repeats; all regions were covered by
            sequence from more than one subclone; and the assembly was
            confirmed by restriction digest.

            MAPPING INFORMATION:
            The sequence of this clone was established as part of a mapping and
            sequencing collaboration between the NHGRI Chromosome 7 Mapping
            Project (Eric D. Green, Director), John D. McPherson in the
            Department of Genetics (Washington University), and the Washington
            University Genome Sequencing Center. For additional information
            about the map position of this sequence, see
            http://www.nhgri.nih.gov/DIR/GTB/CHR7 or send
            mailto:egreen@nhgri.nih.gov

            SOURCE INFORMATION:
            This clone is from a release of the human BAC library. The library
            contains cloned DNA from human sperm. See: Shizuya et al., Proc.
            Natl. Acad. Sci. USA 89:8794-7 (1992); Kim et al., Genomics
            34:213-8 (1996). The clone is available from Research Genetics,
            Inc. (http://www.resgen.com).
            VECTOR:  pBeloBAC11
            Selection: chloramphenicol

            NEIGHBORING SEQUENCE INFORMATION:
            The clone sequenced to the right is RG086D03. The actual start of
            this clone is at base position 1 of RG367O17. This clone is part of
            an unanchored island, orientation is unknown.

            This clone contains STS sWSS1805 (NID:g1113222).
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /chromosome="7"
                     /map="7p15-p21"
                     /clone="RG367O17"
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     repeat_region   1781..2410
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                     (PID:g1346952)"
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     misc_feature    3810..4260
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misc_feature   4217..4745
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repeat_region  5782..6074
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               /rpt_family="ALU"
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Pred. No.:                 0          Length:          79611
Score:                932.00          Matches:           489
Percent Similarity:   23.51%          Conservative:      106
Best Local Similarity:19.32%          Mismatches:        291
Query Match:          15.13%          Indels:           1650
DB:                        1          Gaps:               41

us-09-873-409-5 (1-1222) x AC002486 (1-79611)

Qy    33 CysLeuValGlnThrAsnThrTyrSerPhePheArgLeuThrLeuTyrTyrValGlyIle  52
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Db 56932 TGCTTCAGTCTCCACAATTCTAATAACTCTTTTCTTCAGGTTGACCCTGTATTAATGTTGGAATA 56991

Qy    53 GlyValAlaAlaLeuIlePheGlyTyrIleGlnIleIleSerLeuTrpIleIleThrAlaAlaAla  72
Db 56992 GGTGTTGCTGCCTTGAATTTTTGGTTACATACAGATTCCTTGTGGAATTATAAACTGCCAGCA 57051

Qy    73 ArgGlnThrLysArgIleArgGlyIlePheProHisIleSerSerValLeuValLeuAlaGlnAspIleGly  92
Db 57052 CGACAGACCAAGAGAGAATTCGAAAACAGTTTTTTCATTCAGTTTTGGCACAGGACATCGGC 57111

Qy    93 TrpPheAspSerCysAspIleGlyValLeuAsnThrArgMetThr---------------- 107
Db 57112 TGGTTTGATAGCTGTGACACATCGGTGAACTTAACACTCGCATGACAGAGTAAGAGGATGAT 57171

Qy   107 ----- 107
Db 57172 ATTGTAGTACGTTAGCTTTGTTTTCATATGTGACATGTAAAATGACCTAACTACACATTTATT 57231

Qy   108 --------------------ArgIleAspLysIleSerAspGlyIleGlyAspLysIleAlaLeuLeu 123
            |||||||||||||||||||||||||||||
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Db  57232  TCGTTGTTCAGTTGACATTGACAAAATCAGTGATGGTATTGGAGATAAGATTGCTCTCGTTT  57291

Qy    123  uPheGlnAsnMetSerThrPheSerIleGlyLeuAlaValGlyLeuValLysGlyTyrGly     143
Db  57292  GTTTCAAAACATGTCTACTTTTTCGATTGGCCAGTGGTTTGGTTGGAGGGCTGGAA        57351

Qy    143  sIleuThrLeuValThrLeuSerThrSerProLeuIleMetAlaSerAlaAlaLaAlaCysSe  163
Db  57352  ACTCACCCTAGTGACTCTATCCACGTCTTCCTCTTATAATGGCTTCAGCGGGGCAGCATGTTC  57411

Qy    163  rArg----                                                         164
Db  57412  TAG-GGTAAGTGAGATGGCTAATGCAATATTGAAATGGAAGCAGCAGCGGTGTGGGACTAAATGA  57470

Qy    164  ----------                                                       164
Db  57471  CTCACTGAGTTGTTGTTCAAAAATGGCTTTTCTATTCACTGCCAATTACACAAAG          57530

Qy    164  ----------                                                       164
Db  57531  GGATATTATACACCACAAATACTTTGATTTTGTTCACCATTAATCCCTTTCTATCTTC       57590

Qy    164  ----------                                                       164
Db  57591  AAGTTATTTGGCTAAGATGAAAGTTTTTAATAGCTTACTACATTGAAAAACATTTCTCT      57650

Qy    164  ----------                                                       164
Db  57651  TCATTTAGCAGTCTAACAACACTTCAAGTGGTAGCATGGGATAAAAGTATGATGTCCTTATA   57710

Qy    164  ----------                                                       164
Db  57711  CATGTGATGTTTAGTGTTGCTCGTTGGGACAGACTTGTTTGCTCTAAATTCACAGATCAA     57770

Qy    164  ----------                                                       164
Db  57771  CATGGTACGATTCATTCACTGGGTAGAATGAATAAGAAAATCCTAAAACAATAAACAT       57830

Qy    164  ----------                                                       164
Db  57831  CTTTTATATCATCCTCTTAAAGTTTATGTATATATGTAAAGTTTTTTTTTTTGAGG         57890

Qy    164  ----------                                                       164
Db  57891  CAAGGTCTCACTCTGTCACACAGCCTGAGTGGTGCAAACATGGTTCACTGCAGC           57950

Qy    164  ----------                                                       164
Db  57951  CTCAACTTCCCAGGCTCAAGTCATCCTCCCATCTCAGATCCCAAGTAGCTGGGACTACAG     58010

Qy    164  ----------                                                       164
Db  58011  GCAACCACGCCCAGCTAACTTTTGTATTTTTGTAGAGACAGATTTTCACCATGTTGCCC      58070

Qy    164  ----------                                                       164
Db  58071  AGGCTGATCTCGAATTCTTGGGCTGAAGCTATCCGCCCACCTCGGCCCCACAAACTGCTG     58130

Qy    164  ----------                                                       164
Db  58131  GGATTGCAGGCCAGTGAGCCACCGCGCCCAGCCAAGTTTATACTTCAGTGAAGGCTTTCAA    58190

Qy    164  ----------                                                       164
Db  58191  TTACATTTCAGATTTCTCGCTAAATATCTATTTTTAGTGTACTACACAAATATGTTTCAGTTT  58250

Qy    164  ----------                                                       164
Db  58251  TTTAAACAAATTATGTACTCGCAATTCTAAATTACACATTTTTTAGCACTGTTTTTGCTGTAAGT 58310

Qy    164  ----------                                                       164
Db  58311  ATAACACAAAAATTGTAATCTTAATCTACAGCCTGGTTTTGAAAACGGATACTCTGTGAAATC   58370

Qy    164  ----------                                                       164
Db  58371  TAAAAACAACAAATGTATCTGTAATATTATTTATTCTTCAAAACATATCTTTTTGGAAATTCTAC 58430

Qy    164  ----------                                                       164
Db  58431  CATTGTAATATACTCATCTTCTAGATAGGAGGCACAGTGCTTAAATTTGGCAACACTAAT     58490

Qy    164  ----------                                                       164
Db  58491  CATTCTTTATGGAAATCCAGTGTTCCTAAAATTTCCAGAGTTTATTTACTAACAATATAGTA    58550

Qy    164  ----------                                                       164
Db  58551  ATTCAACAAAACAAGAAATTTTCAGCAATAAAACATATTCTAATAATGGGCTAATCCCTTAACA  58610

Qy    164  ----------                                                       164
Db  58611  ATAGGCTTGGGAGATTGGGACAGCAGTGTCTTTACTTAGTGTGACTCCGAGTGTTGACTTTG   58670

Qy    164  ----------                                                       164
Db  58671  TAGCCTTTATCAAAATCTTCATCCTCAACTTATTTGAAATGAGGAAGGAAATCTCAGTAG     58730

Qy    164  ----------                                                       164
Db  58731  AAAGATTTGCCTGCAGTAAGTAGTTAGTCAGAACCTTAACGTCCACAGAAGAGAAGTAA      58790

Qy    164  ----------                                                       164
Db  58791  ATGAGGAGTTGTAAAGGAATAGAGTGGGGTAGTCTAAATTCTATTATTGTATTCATTGAT     58850

Qy    164  ----------                                                       164
Db  58851  CATGGAGACGAAGCAGGTGAAGGTCAGAGTTATCCAGTGAAGGTCAGAGTTATCCAAAGG     58910

Qy    164  ----------                                                       164
Db  58911  ATGCGGATACCAGAGTGGATGGGCTTCAGCTTCTTCAATTCACTTGACAATTATCTATT      58970

Qy    164  ----------                                                       164
Db  58971  AAATACTTGCTAAGTACAAGGCTTTGTGCCAGGTGGTGTTCCCCTCTAGTGATCTACTA      59030

Qy    164  ----------                                                       164
Db  59031  TAGGAATAATTATCTTTAGTAAGTGAATTCAGAAAATAATGAGTATTATTCCGGCTTCTGC    59090

Qy    164  ----------                                                       164
Db  59091  TACTCTCTCACTTTAACAGTTATCCAAGCACATGTCTTATATAAAATCAGCTCCTATTATGT   59150

Qy    164  ----------                                                       164
Db  59151  GGAATATATTTTTTAGGTGGGAATAGACTTGCTATGCGAATAGGCAATAGTTATGAATTCAC   59210

Qy    164  ----------                                                       164
Db  59211  AGCTCTGAAGGCAGTATCCCGCGTGTTCCCTTTGTGTGGAACTGTGTTGTTAATTACAAAA    59270

Qy    164  ----------                                                       164
Db  59271  TTGTAAAAGGATTATTAAATGGGACATATAAATGGAGAAAAGGGCATGTGAAAATCAGGTAA   59330

Qy    164  ----------                                                       164
Db  59331  ACCTGGTCTAGTCACCAATAGTGATATTTTCCCTTTGTCTCTGAAATCTTACCTCTTAGT     59390

Qy    164  ----------                                                       164
Db  59391  ATTTGAAGACAAAATTTTTAAAAAATACAGAGATAAAGTCTAAAAAAAATACCATTAGTCTAC   59450
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Qy    164 ------------------------------------------------------------ 164
Db  59451 TTAGAATTCAAATTCTGCCTGACTTAAAGTTCAGAAACATTATTACTACAGAGTCATT 59510

Qy    165 ------------------MetValIleSerLeuThrSerLysGluLeuSe 175
Db  59511 TTTTAACTCTGGGTTGTGGTTTATTTACAGATGGTCATCTCATTGACCAGTAAGGAATTAAG 59570

Qy    175 rAlaTyrSerLysGlyAlaGlyValAlaValAlaGluGluValLeuSerSerIleArgThrValIl 195
Db  59571 TGCCTATTCCAAAGGTGGGGCCTGTGGGCAGAAGAAGTCTTGTCATCAAATCCGAACAGTCAT 59630

Qy    195 eAlaPheArgGlnGlnLysGluGluLeuAsnIleThrArgThr 215
Db  59631 AGCCCTTTAGGGCCCAGGAGAAAGAACTTCAAAGGTTCCTTTTAAATAATAACAAGATA 59690

Qy    215 rAlaTrpPheTyrPheProGlnThrpLeuLeuSerCysValLeu***PheValArgThrTyrTh 235
Db  59691 TGCTTGGTTTTATTTCCCCAGTGGCTACTAAGTTGTGTTCTGTT--TTGTAAGGTATAC 59749

Qy    235 rGlnAsnLeuLysArgThrIleAlaSerLysValSe 255
Db  59750 ACAGAACTCAAAAGATGCAAAGGATTTTGGCATAAAAAGCATATAGCTTCAAAAGTGTC 59809

Qy    255 rLeuGlyAlaValTyrPheMetAsnGlyThrTyrGlyLeuAlaPheTrpTyrGlyTyrTh 275
Db  59810 TCTTGGGTGCTGTGTACTTCCTTATGAATGGGAACCTTAGGACTTGGCTTTTGGTATGGAAC 59869

Qy    275 rSerLeuIleLeuAsnGlyGluProGlyLyTyrThrIleGlyTyrThrArgThrValLeuAla 275
Db  59870 CTCCTTGATTCTTAATGGAGAAACCTGGATATACCATCGGGACTGTTCTTGCTGTGAAGTCT 59929

Qy    292 ------------------------------------------------------------ 292
Db  59930 TGTTTGAGAACAAGGTGTCAGGGCCTGGATAATCTTCCTTACCTAGTTTAGCCAAAAATTC 59989

Qy    292 ------------------------------------------------------------ 292
Db  59990 CTCTTTGAAGATAAAATATTCAAAGATGGATGTTTTTATTAAACAAATATTGTTTCCCTC 60049

Qy    292 ------------------------------------------------------------ 292
Db  60050 AAAATTATCTGTATACACCTTTAAATTATTAGTTATTATGAATTGACAGACATTTATTCATCCAGC 60109

Qy    292 ------------------------------------------------------------ 292
Db  60110 ATGTTTTTAGTGTGTCCTCGCTGTGTCAAGACATCTGCATTCCGCTTTGGGAAGAATCATAATT 60169

Qy    292 ------------------------------------------------------------ 292
Db  60170 GAATTCCCACTGGGGAAATACACTGAGTTTGTTGTTAATCTAGCAGTGAAAAAGGCCATTCT 60229

Qy    292 ------------------------------------------------------------ 292
Db  60230 CTTCGTGAGACTTTTCCTTTCATCTCGGGCTGAGATCGAGACCGGAGTTCTGCATTCACCTTGC 60289

Qy    292 ------------------------------------------------------------ 292
Db  60290 TAAAATGTCTTCTCTGGAAATGGTCTGTAGAGTTTACACTCACCTTCCTCTCTGTTC 60349

Qy    292 ------------------------------------------------------------ 292
Db  60350 CTTTTCAGTCATGTAGTAATTTAAAACAGACTACATATAGCTCTGTCCAGTATCACAGTT 60409

Qy    292 ------------------------------------------------------------ 292
Db  60410 TGGAGACTTTTAAATTCTTATGGGTTATGTGTGTTAATAATAATTATTATTCAGTTATATCCTCT 60469

Qy    292 ------------------------------------------------------------ 292
Db  60470 TAAGTTACAATAAACAGATCAGTTCAGGATTAAGAAACATTTGTCTTGAGGAACCAAAAAT 60529
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Db  60530 GATCGCTCTTTATACTTTGATCCTTGTTTGGGCCTTTCCATTCTTACAGATTTCTCTTCT 60589

Qy    292 ------------------------------------------------------------ 292
Db  60590 TTCCATTAAATTCATCTTTTTGAGGGCATTCATAATTAAGACTTTTAGCTATTCAT 60649

Qy    292 ------------------------------------------------------------ 292
Db  60650 TTATTTCATATAAAGTGAAAATGTGAGCATGAACAGATTTTTCCACTCATCCTTGCTCCTCAA 60709

Qy    292 ------------------------------------------------------------ 292
Db  60710 TTTATGTGTGGCTGGGTATCTGGCTTACTAGGCCTAAGCATCCTCATCTTATATGATTAGGA 60769

Qy    292 ------------------------------------------------------------ 292
Db  60770 GTAAGAGCTCCCTAGCTTGAGGGATTCTTTTCTTATTGACTTTTTGCAGGAGATGAGTCTG 60829

Qy    292 ------------------------------------------------------------ 292
Db  60830 TCTTAAAATGGACACAGCTGTCCCCTAATACAAAAATTCAAAAAACGGTTTGAGTGAAAACAG 60889

Qy    292 ------------------------------------------------------------ 292
Db  60890 TACAATGTCTCTGAGCCAATAAAATCTACTGAATTTTCTTTTTAAAGTTCAAGGGGTCA 60949

Qy    292 ------------------------------------------------------------ 292
Db  60950 CCCAACAAGGAGGGGAGTGCAAACTCACCATGGGTTTATACATGGTCAGCACACTTCAGT 61009

Qy    292 ------------------------------------------------------------ 292
Db  61010 TAGCAGAATTTTCTGGTCACACATCCCAGCATGTGATAACCACAAGACTATGAGATAATC 61069

Qy    292 ------------------------------------------------------------ 292
Db  61070 AAAAGTTGTTCCTTATTAGGAAAAAGGCCAAGGATACTTGGATTAATCTCGTGGTTTCTATTG 61129

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Db  61130 CTTCTCGGGCCCTTTGGCTAAGGATCAAGTGTAAATCGTGGTTCTTTTTTATTGGTCATTATC 61189

Qy    292 ------------------------------------------------------------ 292
Db  61190 TTCCATTCTTTCTTTACCTAATTCCTCTAATATCTCTCTGTGGAGCCTAAACCAAATAATTAT 61249

Qy    292 ------------------------------------------------------------ 292
Db  61250 ATATTACATTCTTATGTCTTTCTTTATTAATAACTGCGAAAGATAAAATATCACTTTGTTTGT 61309

Qy    293 ------------------ValPheSerValIleHisSerSerTyrCysIleGlyLyAlaAlaValProH 310
Db  61310 TCCTGTAGGTTTCTTTAGTGTAATCCATAGCAGTTATTGGATGGACAGCAGTCCCTC 61369

Qy    310 isPheGluThrPheAlaIleAlaArgGlyValAlaAlaPheHisIlePheGlnValIleAsp 329
Db  61370 ACTTTGAAACCTTCGCAATAGCCCGAGGAGTCGCCTTTCATATATTTTCCAGTTATTGATA 61429

Qy    329 ------------------------------------------------------------ 329
Db  61430 AGGTAAGACCTTCTTATTGCTTTGAAGAATAACTATCATTACTGCAAGGAGGAGACAAAAA 61489

Qy    329 ------------------------------------------------------------ 329
Db  61490 AACATTACACCCTCATTTTCACTAAAACAATAGGATGGACAAATTTAATGTTGGCCAGTTG 61549

Qy    329 ------------------------------------------------------------ 329
Db  61550 TTTATGGGAAAGAGAGAGACTGCCCTTTAAATTCTTTCTTTTTAAGAGGAGAGTTGTGTTGTATTGAA 61609

Qy    329 ------------------------------------------------------------ 329
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Qy    902  eArgPheGlyAlaTyrLeuIleGln----AlaGlyArgMetThrProGluGlyMetPheIl  921
           |||:::::::|||:::::|||:::                           |:|||||
Db  63428  GAGCTTCATTAAATAGCTTGTGAAAATATCTGGCAAG------------------AT  63466

Qy    921  eValPheThrAlaIleAlaTyrGlyValMetAla---------------------------  932
           ||||||||||
Db  63467  CTCATTACTTGTTTACAAATTAAGACTTCATTAACTTGATAGTCAAAATTCATATAAAA  63526

Qy    933  -----------------IleGlyLysThrLeuValLeuAlaProGluTyrSerLysAlaLy  947
                            ::|                  :::||||||
Db  63527  TATTTTAGTTGAAAATGTGAACAGTTTACTTAGTTATAATATTCTGAAGTACTCTTAATTAG  63586

Qy    947  sSerGlyAlaAlaHisLeuPhe-------------------AlaLeuLeuGluLysLy  960
           |||:::                            ------
Db  63587  TTTCT--------CTTTACATAGAGAGATAAGTGAATAGATTCTTTACTACTATTTTC  63634

Qy    960  sProAsnIleAspSerArgSerGlnGluGlyLysLysProAsnThrCysGlyAsnIle  980
           |||                   :::                  :::
Db  63635  TGAAATTATTCAGCCTATTACTACACATGTACATGAAACAACAAGACTAAAATT  63694

Qy    980  uGluPheArgGluValSerPhePhe-Tyr---------------ProCysArgP  993
           |||||                       :::
Db  63695  TGTTTTAGAAGAATTTGTTTTTGGTTATATAATTAATGTACTCATTTTCTGAAAATGTGTCC  63754

Qy    993  roAspValPhe-----------------------------------IleLeuArgG  1000
                                                      ::|||
Db  63755  ATCACTCTTCTTATTGTGGTTTTATGATTTTCCCTCCCATACATTCCAATAGATTCTGAAAG  63814

Qy   1000  lyLeuSerLeuSerIleGluArgGlyLysThrValAlaPheValGlySerSerGlyCysG  1020
           ||||:::        |||:::                  :::||
Db  63815  GTCTGAAATCTCAGAAATTAAGTCTCTGGAGAGACAGTGGCCTTGGTCTCGGTCAATGGCAGTG  63874

Qy   1020  lyLysSerThrSerValGlnIleLeuGlnhArgLeuTyrAspProValGlnGlyGlnValI  1040
           |||||||||||||||||||||                  :::
Db  63875  GGAAGAGTACGGTAGTCCAGCTTCTGCAGAGGTTATATGATCCGGATGATGGC--------  63927

Qy   1040  euPheAspGlyValAspAlaLysGluLeuAsnVal-------------------------  1051
           ||:::                            ::::::
Db  63928  --TTTGTAAGTGCAGCTAGCAAAACCATGCACGTCCACCTAATGGAAATCTGGAAACACC  63985

Qy   1052  ------------------------GlnTrpLeuArgSerGlnI  1058
                                   |||||||
Db  63986  GCAGGGCCTGGCACCTGCTGTAACTTTTCATTTTCAACAGTAGAGCTGGGAGAGAAGCCATA  64045

Qy   1058  leAlaIleValProGlnGluPro  1065
           |||                 |||
Db  64046  TTGTTTTCTTTCCTTTGTATCCA  64068
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OM protein - nucleic search, using frame_plus_p2n model

                GenCore version 5.1.6
                Copyright (c) 1993 - 2003 Compugen Ltd.

Run on:         December 17, 2003, 15:11:26 ; Search time 129 Seconds
                (without alignments)
                2.277 Million cell updates/sec

Title:          us-09-873-409-5
Perfect score:  6159
Sequence:       1 MILGIIASLVNGACLPLMPL..........QELLRNRDIYFKLVNAQSVQ 1222

Scoring table:  BLOSUM62
                Xgapop   10.0 ;  Xgapext   0.1
                Ygapop   10.0 ;  Ygapext   0.1
                Fgapop    6.0 ;  Fgapext   0.1
                Delop     6.0 ,  Delext    0.1

Searched:       1 seqs, 120169 residues

Total number of hits satisfying chosen parameters:   2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1 summaries

Database :      4827303_1999:*

Command line parameters:
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-SUFFIX=pto -OUT=align5_1999 -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits
-START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO_XLPXY
-NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.


                                 SUMMARIES
                            *
Result    Query               Match  Length  DB  ID
  No.     Score                                          Description
  ----    -----               ----   ------   --  --       -----------
c  1    1739.47    28.2    120169    1   AC005060    ACCESSION:AC005060


                                 ALIGNMENTS

RESULT 1
AC005060/c
LOCUS       AC005060           120169 bp    DNA    linear    PRI 14-MAY-1999
DEFINITION  Homo sapiens clone RG086D03, complete sequence.
ACCESSION   AC005060
VERSION     AC005060.2  GI:4827303
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 120169)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 120169)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUN-1998) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   3  (bases 1 to 120169)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAY-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     [WARNING] On Oct 2, 2000 this sequence was replaced by a newer
            version gi:10445386.
            On May 14, 1999 this sequence version replaced gi:3212931.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="RG086D03"

us-09-873-409-5 (1-1222) x AC005060 (1-120169)

Alignment Scores:
  Pred. No.:                    0
  Score:                        1739.47          Length:          120169
  Percent Similarity:           6.47%            Matches:            838
  Best Local Similarity:        5.46%            Conservative:       155
  Query Match:                  28.24%           Mismatches:         227
  DB:                           1                Indel8:           14147
                                                 Gaps:                20

Qy     1 MetIleLeu----------------------------------------GlyIleLeu---------Ala  7
           |||||||||                                      |||:||:|||   |||
Db 70326 ATGATCCTAGTTCACTGCACCTCAAACTCTTGGCCTGAAGGGATGGCTTCCACCTCAGCC 70267

Qy     8 SerLeuValAsnGlyAla---CysLeuProLeu------------------------------  17
           ||| |||||| |||||                |||                 |||
Db 70266 TCCCAAGTTAGCTGGAACCAGCAGGTGCACGCCCACTGTGCCCTGGGCTAATTTTTCATTTTTATG 70207

Qy    17 -----------------------------------------------------------Glu 24
                                                                       |||
Db 70206 TAGAGACAGAGTCTTGCATGGTTGCCTAGGCTGGTCTTGAACTCCTGGGCTCAAGTGATC 70147

Qy    18 MetProLeu---------------------------ValLeuGly--------------------  23
           :::|||||                            ||||||||
Db 70146 CTCCCACTTGGGCCTCCCAAAGTGCTGGGATTATAAGTATGAGCCACCGACCCAGCCTA 70087

Qy    24 ------------------------------------------------------------- 24
Db 70086 GAGCGAGCTATAATCTTTTTTTTTTTTTTGAGACAGTCTTCTCTGTCACCCAGGCTGGAG 70027

Qy    25 MetSerAspAsnLeuIleLeuSerGlyCys------------------------------- 33
           :::::::                      :::
Db 70026 TGCAGTGGCGCAGTATCTCATCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGACTCTCCT 69967

Qy    33 ----------------------------------------------------------- 33
Db 69966 GCCTCAGCCTCTCAATTAGCTGGGACTACAGGTGCCCACCACGCGCCCAGCTAATTTTT 69907

Qy    34 ----------------LeuValGlnThr------------------------------- 37
                           ||||||||:::||||
Db 69906 GTATTTTTAGTAGAGACGGGGTTTCACCGTGGTTGGTCAGGCTGGTATCGGAACTCCTGACC 69847

Qy    37 ----------------------------------------------------------- 37
Db 69846 TCTCGGTGATCCTCCCACCTCGGCCTGTAATCCCAAAGTGCTGGGATTACAGGTGTGAGCC 69787

Qy    37 ----------------------------------------------------------- 37
Db 69786 ACCGTGCCCAGCTGAACTATAATCTTTAAAGTTAATAGAACACAGAAACACAGAAGGTAGT 69727

Qy    37 ----------------------------------------------------------- 37
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Left column:

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Db  69726 GAGGAATCAGGAACTATATTATTATGGTTACCTAATAGGAGAGATATCCAAACAGAAAAGAATAA 69667
Qy     37 --------------------------------------------------------------- 37
Db  69666 CTGCCCCAGTGGATATGTTTTTATCCTTTCGACAATATAGATACTGTGCCAAGAATGAAA 69607
Qy     37 --------------------------------------------------------------- 37
Db  69606 TCCAAAAAGTAAAAATCATTGGCTCAAAATATTAAAAGAAACTTCCAAGTGGGAAATTA 69547
Qy     37 --------------------------------------------------------------- 37
Db  69546 ATACAGTATCAAGGTCTACAAAAACATAACCCCTTATCAAGTAATCAACAGTAATT 69487
Qy     37 --------------------------------------------------------------- 37
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Qy     37 --------------------------------------------------------------- 37
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Qy     49 -----TyrValGlyIleGlyValAlaAlaLeuIlePheGly--------------- 60
Db  69366 AAAATTTTATGTAGCTATAGGAGCATTAGTATTATTTTTTAGGAGCACTTTCCAGGAACCAA 69307
Qy     61 --------------------------------------------------------------- 61
Db  69306 GGGCAAAGACAGCAAATTTTTTTTTATTGTACCCCAGATTTTAAACAGTACTTAGTGGGA 69247
Qy     61 --------------------------------------------------------------- 61
Db  69246 CATTTTTAAGGGATAAACACAAAAGCATTACCATATAGTTTTCATGGACACACTTATATGC 69187
Qy     61 --------------------------------------------------------------- 61
Db  69186 ATTAATAAAACATTAAAGATGTAAATTGTGGGGACACATGTATATCCAAATTCAAAAAGACCATAGTAA 69127
Qy     61 --------------------------------------------------------------- 61
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Qy     61 --------------------------------------------------------------- 61
Db  69066 AAAAGCAACAAAAATTTGAAAACAGGAGACCCTTGTCATTTCCCTAGAAGAGAAAACTGGACA 69007
Qy     61 --------------------------------------------------------------- 61
Db  69006 ATCTAGGAGTTCATTCAGAAAAAGCAAAGTGGGTGAGGGCTGAAACCTTACAGCCTGTTAGC 68947
Qy     62 -IleGlnIleSerLeu------------------------------------------ 48
Db  68946 AATACAGCTTTCCCTTAGGAATTCTAAAGCGTGCCGAACCCCAGCGGCCAGCCTTAGGGAAT 68887
Qy     66 --------------------------------------------------------------- 66
Db  68886 CTCCTTTCGCCATCTACTGATTCCCCAGCGATCTCCTCCAGTCCCAAGGCTTAGATGATGGC 68827
Qy     66 --------------------------------------------------------------- 66
Db  68826 CAAACACCTACCGACAAAAGCCCAGGCTTACCCGACCTGAACGGCCACACTC 68767
Qy     66 --------------------------------------------------------------- 66
Db  68766 CAGACTGGTCTCTCCCATCTGGAGCTTGAGATGACCCGCACCAGGAGCATTAGTATTTA 68707
Qy     66 --------------------------------------------------------------- 66
Db  68706 AGGAAAGACATTGGAAGGCCTCCACAAATGCCAAGAACTTAAGGTCCACAGCGATCTCACCG 68647
Qy     67 --------------------------------------------------------------- 67
Db  68646 GTTGTCTCTAGTCCATATGACTCTGAAACTTATTGGGTGGGGGTCTGGGGAGGCAGGAGGCAAGG 68587
Qy     67 ----------------Trp-------------------------------------------- 67
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Right column:

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Qy     68 ----IleIleThrAlaAlaArg-------------GlnThrLysArgIleAr 79
Db  68586 ACAGTGTGTTAG--TCAGCTCGGGCGGCTTCCATAACAAAAGGACCACAGACTAGGAGGTGCA 68529
Qy     79 glyGlnPhePheHisSer------Val----AlaGlnAsp--------- 90
Db  68528 ACAACAGACATTCATTTCCTTACAGTTCTGGAAAGCCACAAGAAGACAAAGAGAGTCCG 68469
Qy     91 ----IleGly------------------TrpPheAspSer--Cys---- 97
Db  68468 CACGAATTGGGTTTTACTCGGAGGGCCTTGGCTTTGGGCTGTGTTCTATTGCGTCCTC 68409
Qy     97 --------------------------------------------------------- 97
Db  68408 ACAGGAATCTTCTCTGTGTATGTCAGTGTGTCTGCGTGTGTCCAGATTTCCTCTTTTTTTT 68349
Qy     98 -----------------------------------------Asp-------I 99
Db  68348 TTTTTTCTTTTGGAGCAGACTTTGCTGTCTCCCAGGCCTGGACTGCAGTGGGCGGTTATG 68289
Qy     99 leGlyCysGluLeu--AsnThrArgMet------------------------ 106
Db  68288 TTGGCTCACTGCAACCTCCGGCCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGCGTCCTGA 68229
Qy    107 --------------------------------ThrAsp-------------- 108
Db  68228 GTAGCTGGGATTACAGACAGCAGCCACCATGCCCGGCTAATTTATTTTTAGTAGAGATGA 68169
Qy    109 ----------------IleAspLys---IleSerAspGly------------ 117
Db  68168 GGTTTCACCATGTTGATAAGGCTAGTCTCAGAACTCCTGACCTCAGGTGATCCGCCCGCCTCG 68109
Qy    117 ----ly-AspLysIleAlaLeuLeu------------------------- 126
Db  68108 GCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCAAATTTCCTCTT 68049
Qy    127 MetSerThrPheSerIleGlyLeuLeuAlaValGlyLeu--ValLysGlyTrpLysLeuThr-- 145
Db  68048 CTTACAAGAATATCTATACAGTTAGAATTAGAGCCTTAAAAACTTCACTTTAACTTA 67989
Qy    146 --------------------LeuValThrLeuSer------------------- 150
Db  67988 ATTATCCCGTATCTATAAATTATTATTATTCCAAATACGGTAACA 67929
Qy    151 --------------------------------------------------------- 151
Db  67928 TTCCTTGTAACATTCTTTTTTTTTTTTTTTTTTTTTTTTTGAATACAGAGAGC 67869
Qy    153 roLeuIleMetAla------SerAlaAlaCysSerArgMetValIleSerLeuleuTH 170
Db  67868 CTCGCGTCTGTGCCCAGGCTGGAGTGCAGTGGCGCGAATCTCGGCGTCCATTGCAAGCTCCAC 67809
Qy    170 rSerLysGluLeuSerAlaTyrSer------------------------LysAlaGlyA 182
Db  67808 CTCCC--GAGTTAACGGCCATTCTCCTGCCTCCAGCCTCCAGTAGCTGGGACTACAGGCG 67751
Qy    182 la--------------------------------------------ValAlaGlu------ 185
Db  67750 CCCGCCACCACGCCTGGCCTAATTTTTTTGTGGTTTTTTAGTAGAGACGGGGTTTC 67691
Qy    186 GluValLeuSer------------SerIleArgThr----------------- 193
Db  67690 ACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCAGGTGATCCGCCCGCCTCC 67631
Qy    194 ----ValIleAlaPheArgAla------------------------------- 199
Db  67630 CAAAGTGCTGGGATTCCAGGCGTGAGCCACGGCGCCCAAATACAGTAACATTCTG 67571
Qy    200 --------------------------------GlnLysGluLeu--------- 206
Db  67570 ATAAACTGGAGAGGTTAGACCTAAACAATAAAAATGTAGGGGTCGGAGGGACACAATGTAGGCCT 67511
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Qy    207 ------------------------------SerPheLeuLeuAsnIleThrArg------------- 214
                                        |||  :::|||
Db  67510 ATAACATACACCACCATTTATCTCTTTTATCCTTTAAACTTCC-AGGGGATGAACTGTGTAAG 67452

Qy    215 -----------------------TyrAla--------------------------------------- 219
                                  |||
Db  67451 TCAGCATTATATGCCAAAATGGCATCCCCATTTAGGCCCATTTGCTTAGAGTTAGTGTGTAT 67392

Qy    220 --PhePro----------------------------------------GlnTrp------------ 223
             :::|||                                     |||
Db  67391 CATACCCTTAAACACTTAACCAGGCTACCTTGTTGTCGATCTTAGTTTTCAGTATTTCATAGT 67332

Qy    224 ------LeuLeuSerCysValLeu***PheVal--------------------------------- 232
              ||||::       |||:::
Db  67331 TTTTTGAGTGTTTTGCTGTTGTGTGGTTTTTAAATTTCCTTAGATGTTTTAGT 67272

Qy    233 -------------------------ArgTyrThrGlnAsnLeuLeuLysAspAlaLys------- 242
                                     |||:::
Db  67271 GAGAAAATGGGAAAAATGGTTGAGTCATCACCAGATACAGTCTTCGAAACCACAAAG 67212

Qy    243 AspPhe-GlyIleLys-ArgThrIleAlaSerLysValSerLeu---Gly---------------- 257
          |||      |||:::                              |||
Db  67211 TTTTTTAGGGAATTAGGCAGAGCCCTGGGGGGAGGGGAGGGATTTGTTATGGTTATTTTTA 67152

Qy    257 --------------------------------------His------------------------- 257
                                                  :::
Db  67151 ATGAAGATGCTAATTTTTTATAGTTTCGGTGAAAATTGATGTAATACTTTTAGGGAAGCAA 67092

Qy    258 --------------------AlaValTyrPhePheMetAsnGlyThrThrTyrGly---------- 268
                               |||:::
Db  67091 TTTGGCAATACCCATCAAGAAGTAAGTATACACCTTTTTAAATTTCTTCAGAGGT 67032

Qy    269 Leu--AlaPheTrpTyrGly-----------------------ThrSerLeuIle----LeuAsnGl 281
          |||                 :::|||                                |||
Db  67031 TTATAACCTGTTACTATATAATCATTTATTTTGACTCAAATTATCCCAGATTCAGCCAGTGG 66972

Qy    281 yGluPro------------------GlyTyrThrIle---GlyThrVal---------------- 290
           :::|||                  |||               |||
Db  66971 AAGTCCCTTCAAGTTGGGAGAATTACACCTTTTAAGGTGTAATTCCAGTTAGAAAATTTAA 66912

Qy    291 ----------LeuAlaVal-----------------------PhePhe----------------- 295
                    |||:::                         |||
Db  66911 CAATAGGGCATTTGAGGTGTAAGTAGGGTTGTAAATGAGAACAAAAGATTTTTCACAAAGATGT 66852

Qy    295 ----------------------------------CysIleGlyAlaAlaVal-------------- 308
                                             |||
Db  66851 TCATTACATCTTTATTTTTAATAACGAAGGCAACCCAAATTGAAGGCAACCCAAATATTT 66792

Qy    296 -----------SerValIleHis------------------SerSerTyr-------------- 302
                      |||:::                       |||
Db  66791 TTGGAGAATATTTAATAACTGCAGTAATAGTTACAAGGAATAAATCAGGATACAAACTG 66732

Qy    309 ----------------------Pro------His------------------------------ 310
                                  |||      |||
Db  66731 CATGCACGTAATAAAACCAAAATCTGAATCTGTATAAGTATTANTGTCTCAGAAGCCATGTAGA 66672

Qy    303 -----------IlePheGlnValIle--------------AspVal------------------- 308
                      |||:::                      |||:::
Db  66611 ATTTCAAACTGTCGGTCAATTCTCTGTTTCCAGTGAAAATAGGGGCCCTCATTTTTTTTTTAA 66552

Qy    311 --PheGluThr--------------PheAlaIleAlaArgGlyAlaAlaPhe------------ 322
             :::|||                |||
Db  66551 TCCCAGCACTAAAGAACTTAGTTTCAGCTAATTTGCTAAATATCATACATCCCCACTGA 66492

Qy    323 --------His--------------IlePheGlnValIle-----AspThr------------ 330
                    |||               |||                |||
Db  66491 AAGATGATCCAATAA--AATGTGTAGTTCTTATAAAAGTTATAAAAGATAATTCTACATATT 66434

Qy    330 sLysProSerIleAspAsnPhe----SerThrLeuGlyTyrLysProGlySerIleGluG 349
           :::|||              |||||              |||:::|||
Db    349 lyThrValGluPheLysAsnValSerPhe-AsnTyrProSerArgPro--SerIleLysI 368
```

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Db  66433 TGAAGGTAT---TTTAAAAAATTTATTTTACCTCATACT--ATGACTCCTTTTCTATCTTGA 66378

Qy    368 le------------------------------LeuLysGlyLeu--------------------- 379
                                           |||:::|||
Db  66377 TATTGCCTCTTAGATCTTTTACTGAGTGAAACCAATTTATAAATGTGCAAAAATGGGAATGA 66318

Qy    380 --GluThrValAla----------------------------LeuValGlyLeuAsnGly---- 389
             :::|||                                 :::|||
Db  66317 GAGAAAATCGTATCCAAAAGTATACACTTTAAATGAATATCATAATCATTCAAACTCAACACT 66258

Qy    390 --------------------SerGly-LysSer---------ThrVal---------ValGlnLeu 398
                               |||                   |||            |||
Db  66257 ACTATAGATAGAGTGGCTAAGAGTGCCTTCCGTCAGTGTGGGAAAGGGGTAGGGCTG 66198

Qy    399 ----------------LeuGln----ArgLeuTyrAsp------------------------- 404
                            |||        |||
Db  66197 GGGGTTTGCAGCCCCCGGATATTATGACACCCAGTGTGGTGGCAGCCCCGTGCAGGGAAGCAG 66138

Qy    405 --ProAspAspGly----------------PheIleMetValAspGlu--AsnAspIleArgAla 419
             :::|||                      |||:::
Db  66137 AGCCAGACGCAGGGTGAGAGAAGCGGGTGTTCCGTGCAGG--GAAGAGGCAGCAGGAGCAGCA 66080

Qy    420 LeuAsnValArgHisTyrArgAsp-----His------------------------------- 429
          |||                         :::
Db  66079 GA-TGGGGTTACCCATGG-AGAGATTAAATCACATAGATCAATCATTATTAAAGACAATGGGAG 66022

Qy    430 --------------------GlyValValSerGlnGlu-------------------------- 435
                               :::    |||
Db  66021 CCAGTTTCTCCCTTGTGTGAAGAGGGGTATAACAAAATATGGAAAAAGGAGAAAAACTCGAAAT 65962

Qy    435 ------------------------------------------------------------------ 435
          
Db  65961 AACCTTACAAATGTTGACTTGGAATTGGAGTATGACTCATCATGAGTTTCAAGAAAT 65902

Qy    436 --------------------Pro------------ValLeuPheGlyThr------------- 441
                               |||              :::|||
Db  65901 ATACAGAAACAAATATAGATGTAAAGTGTGTTGTTACCTTATCAATACACACACACACAC 65842

Qy    442 --------ThrIleSer--------------AsnAsnIle--------------------- 447
                  |||                   |||
Db  65841 ACACACACACACACCATTCTCTAGTCTGCACCACTGAATTCTAGTTATTAATGAGTAGACAAC 65782

Qy    448 -------------LysTyrGlyArgAsp---------------------------------- 452
                      |||:::|||
Db  65781 CAGCACCATATCTTGACTGCTAAATAAAATTCTCCACTAAAAGAACACCAGGACTCTTTGG 65722

Qy    453 -----------AspVal--------------ThrAspGluMetGluArg------AlaA 463
                      |||:::                |||
Db  65721 AGAAATGACTAATTCCAAAAGTAGGGCACAGTACAAGATGAAAACTGGAAAAATCATT 65662

Qy    463 lAArgGluAla------------------------AsnAlaTyr------------------ 469
          :::|||                             |||
Db  65661 TTTGTCTCAGAAAGTAAGGACATAATTCCAAAAACTCGATAGGTTATAGTCAAAAGGACAAAGCC 65602

Qy    470 Asp--------------------------------------PheIleMetGlu------- 474
          |||:::                                   |||:::
Db  65601 AACGTGAAGGGACTTCCCACTCGGCTACATCTGGGATAATTGAGTCAAAATAAATGATTAT 65542

Qy    475 --PheProAsnLys-------------------------PheAsnThrIle---------- 482
             :::|||                             |||
Db  65541 AGTAACAGGTTATAAACAACTGAGAGAAATTTAAAAGTCATTAGTTCATTACTACAAAAT 65482

Qy    482 uValGlyGlyLysGly----AlaGlnMetSerGlyGlyGln----LysGlnArgIleA 499
           :::|||              |||:::|||                |||
Db  65481 AAGTTGAAAGTTTGATGAGAATGGATTTTTGACATAGTTCTTTGACTAGTTGCTTCAAGACATT 65422

Qy    499 laIleAlaArgAlaLeuValArgAsn------------Pro---LysIle-LeuIleL 513
          |||                                  |||:::  :::|||
Db  65421 TATTAATTACAAAGGGAGGAGAAAGAACAACTTCATAGCGGAGAAAAACCATCT 65362
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Qy     767 ---------------------------------------------------------- 767
Db   63159 GCGAAACCCATCTCTACTAAAAATATAAAAAAATTAGCTGGGCGTTGGCGGGTTGGCCT 63100
Qy     767 ---------------------------------------------------------- 767
Db   63099 GTAATCCCAGCTCTCCAGAGGCTGAGGCAAGAGAAATGGCTTGAACCCAGGAGGTCGGAGG 63040
Qy     767 ---------------------------------------------------------- 767
Db   63039 TTGCAGTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGTGACAGAGTGGGACTCCAT 62980
Qy     768 ---------------------------------------------AlaGln- 769
Db   62979 CCCGGAAAAAAAAATAAAATAAGTAAATAAATAAAAAATATGTATCTTATTTAATCTCAAA 62920
Qy     770 ---IleGlnGly- 772
Db   62919 GTATAAATTCAAGGCATAAAATTTAAGTATAAAATTCTTTTTTAAAAAGTCTACCTTGTTT 62860
Qy     772 ---------------------------------------------------------- 772
Db   62859 TGCAAGGAACTATATAATAGGAACTCTTGTAAAATGTAAAGTTAATTGAGTTTTTCCCCAA 62800
Qy     773 ------AlaThrGlySerArgIleGlyValLeuThrGlnAsnAlaThrA 787
Db   62799 AATATGTCTGATTATAGGCAACAGGTTCCAGGATTGGGCGTCTTAAACACAAAATGCAACTA 62740
Qy     787 snMetGlyLeuSerValIleIleSerPheIleTyrGlyTrpGluMetThrPheLeuIleL 807
Db   62739 ACATGGGACTTTCAGTTATCATTTCCTTTATATATGGAAGAGAATGACATTCCTGATTC 62680
Qy     807 euSerIleLeuAlaProValLeuAlaValThrGlyMetIleGluThrAlaAlaMetThrGlyP 827
Db   62679 TGAGTATTGCTCCAGTACTTGCCCGTGACAGGAATGATTGAAACCGCAAATGACTGGAT 62620
Qy     827 heAlaAsnLysAspLysGlnGluLeuLysHisAlaLaGly- 839
Db   62619 TTGCCAACAAAGATAAGCAAGAACTTAAGCATGCTGGAAAGGTAAAATGAAGACTGTTAT 62560
Qy     839 ---------------------------------------------------------- 839
Db   62559 CACCATCGTAACATTTAAAGAGAAAAACAGTCAGAACTTTATGATATGTTAACTATATGA 62500
Qy     839 ---------------------------------------------------------- 839
Db   62499 TGTGTTAACCATCTTTATGATATATTAACTTCATCTCTTAGGGATCTGTAAAGTAAGATATG 62440
Qy     839 ---------------------------------------------------------- 839
Db   62439 TATAGAGAGAAAATGCATACAGACCAATTTACGATAGAAGGTAGATATGTTATAGCAAT 62380
Qy     839 ---------------------------------------------------------- 839
Db   62379 AGGGTACATGATTTAGAGCACAGGCTCTCGGAGTCTAATTAGCTGAGTTAGAATCCAGATT 62320
Qy     839 ---------------------------------------------------------- 839
Db   62319 CTATGCTAACAAACGTGTGATATGAGCAGGTTATGTCAACCTTTGTACTTCAGGTTTC 62260
Qy     839 ---------------------------------------------------------- 839
Db   62259 TCATCTGCAAAGTGGGAATAATACGAGTATTCACTTACAAAATTTTTGTGAATAATTGCATA 62200
Qy     839 ---------------------------------------------------------- 839
Db   62199 AAACACAATGTTATTATACGGCAAAACACTTAGAACAGTGTCTCGGAAGACAGTAAGCACGT 62140
Qy     839 ---------------------------------------------------------- 839
Db   62139 ACTAAGTTCAGCCATTATTACTGGGGAAGTTTCAAAACATCATCATCATTCCCATTTTCTGG 62080
Qy     839 ---------------------------------------------------------- 839

Db   62079 TCATTGAATAATCAAATTTTCTTGAGCAATTCTTCTGAATATATTTTATTTTTCAAAACAA 62020
Qy     839 ---------------------------------------------------------- 839
Db   62019 CAGGCAAATGCAGCAGTTACTGAATGCAAGGCCATGCACTGATATTGATAACATAAAAC 61960
Qy     839 ---------------------------------------------------------- 839
Db   61959 AAGGCTTTAGAGACAGGACCAATAAATGACCAAATTTATTTTAATCATTGTGAAAAATGCCTGG 61900
Qy     839 ---------------------------------------------------------- 839
Db   61899 ACATACAGGTATTTAAGCTTCTTAGGGATCAACCATATATTCATACAAAATAATTAATTATTA 61840
Qy     839 ---------------------------------------------------------- 839
Db   61839 GAGACTGAAGGAAACATTATGGTGGCATCATAACACCTAAGAATTGAAAAGAGAACATCATC 61780
Qy     839 ---------------------------------------------------------- 839
Db   61779 TGACCCAACCATTAACCTGAAGTAGGAGGTCCCTTGCACAACATCCCTGTCAAGGGTCCAT 61720
Qy     839 ---------------------------------------------------------- 839
Db   61719 CCCCATCTCCTACCACCTTTTCCTCCAGTGGGCAGGTAGTAGTACATTACTTCCCAGGCTGCC 61660
Qy     839 ---------------------------------------------------------- 839
Db   61659 TGTACTTGGATAGTCTTGGGTGGGTAGGCAGTTCTTTTCCTTTTTCTTTTTCTTTGT 61600
Qy     839 ---------------------------------------------------------- 839
Db   61599 CTTATTTATTTATTTATTTATTGGTTGGGACTTCTATCCTTACTCTCTTGGCTTTCATCTTG 61540
Qy     839 ---------------------------------------------------------- 839
Db   61539 GTAGAGGTCCAAAATCTGTTTTTCACGACAGCCCTTTAGCAGCTGAAATCGGCTGTGTAAAACAA 61480
Qy     839 ---------------------------------------------------------- 839
Db   61479 GGAGACTTCTGTTGACTCTACATCCAGGTCTTTAAGATGTTCCTCACACCTGTAATCCCA 61420
Qy     839 ---------------------------------------------------------- 839
Db   61419 GAACTTTGGGAGGCCGAGATGGGCGGATCTTTTGAGGTCAGGAGTTTGAAACCAGCCTGG 61360
Qy     839 ---------------------------------------------------------- 839
Db   61359 CCAACATAATGAAACCCCATCTCTACGAAAAAATACAAAAAGTTAGCCGGGGTGTAGGGTG 61300
Qy     839 ---------------------------------------------------------- 839
Db   61299 CGTGCCTGTAATCCCAGTTACTTGGGAGGCTGAGGCAGGAGAATCACTTGAACCCAGGAG 61240
Qy     839 ---------------------------------------------------------- 839
Db   61239 GTGGAGGTTGCAGTGAGCTGAGATTGCACCACTGCACTCCAACTTGGGCGACAGAGCACA 61180
Qy     839 ---------------------------------------------------------- 839
Db   61179 GCTCTGTCTCAAAAAAAAAAAAAAAAAGGGTGTTCCTCTCCTAATACTGTGTTTCAGA 61120
Qy     839 ---------------------------------------------------------- 839
Db   61119 GCTCTTGGGCTACACTGGTGTACATCCTCTGAATAGGCAAAATGATGTTAATATCCTTTATA 61060
Qy     839 ---------------------------------------------------------- 839
Db   61059 GTCTGTATCACGGTTGGAATGTTGTCACAATTGGCATAGCATTAAAAAGTCATTACACATATTCATGA 61000
Qy     839 ---------------------------------------------------------- 839
```

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Db   60999  ATAGGGATGCCAAGCACATAACTCACTGTAATCTCGTTTGCCTGAGCCTTAGACTTTCC   60940
Qy     839  ------------------------------------------------------------     839
Db   60939  ACCTTTTTTTTGCACAAGATAAGGACCCTTGGATTGTTGCTTGTGTCGTATAGTCTGAAC   60880
Qy     839  ------------------------------------------------------------     839
Db   60879  TACCTAGCAAATATTGCCTCAGAGACAGTAAACAGTTGTTTAGACCTCCTTGTCTAATT    60820
Qy     839  ------------------------------------------------------------     839
Db   60819  TAAACATTGCAATAATTATTATACAATTTCTAAATTAATTAATTATGTTTTCCTCA       60760
Qy     839  ------------------------------------------------------------     839
Db   60759  TCTTATTTTTTATGTCATGAGCTTTTGCTGTATATGTTGCCCTTTGACTTTTCTTTATGT   60700
Qy     839  ------------------------------------------------------------     839
Db   60699  ATCATTAGAGCAACCTCAGACTATACAAACAACTCTAATCAAATAGTCAATTGGAGG      60640
Qy     839  ------------------------------------------------------------     839
Db   60639  CATTTCCCTATGGCTTTTAATAAGTCAATTTACTAAACATCAATTTAGAACATAGACTAA   60580
Qy     839  ------------------------------------------------------------     839
Db   60579  TAAAATGTATCGGTCCTTCTTCAGTTGCATGTGAGATTGGGAAAAATTATCAAACGTTT    60520
Qy     839  ------------------------------------------------------------     839
Db   60519  AGTTTTTAAGACTTTGAATGGGCCAGGTGCGCTGGCCTTACGCCCTGTAAATCCCAACACTTT  60460
Qy     839  ------------------------------------------------------------     839
Db   60459  GGGAGGCCGAGGCAGGTGGATCACAAAGGTCAGGAGTTCGAGACCAGCCTGACCAACATGG   60400
Qy     839  ------------------------------------------------------------     839
Db   60399  TGAAACCCTGTCTCTACTAAAAATACAAAAATTAACCAGGTATGGTGGCACACGCCTGCA   60340
Qy     839  ------------------------------------------------------------     839
Db   60339  ATCCCAGCTACTCAGGAGGCTAAGGCAGGAGAATCACTTGAACCCAGGAGGCAGAGGTTG   60280
Qy     839  ------------------------------------------------------------     839
Db   60279  CAGTGAGCCAAGATCGCACCACTGCACTCCAGCCTGGGCAACAGAGCAAGACTCCATCTC   60220
Qy     839  ------------------------------------------------------------     839
Db   60219  AAAAGAAAACAAAAAAAGACTTTGAAATAGCTTAATTAGTTTTCTTAAATGACTATTTCTA   60160
Qy     839  ------------------------------------------------------------     839
Db   60159  AGGGTCTGTAATAATATTCATCCCTTCTCCATTGTGAAAAATTGGAGATTTTTTTAATGT   60100
Qy     839  ------------------------------------------------------------     839
Db   60099  TCATTCCTTTTTTTTATCTTGTTTTTCCTCAAAAATTTTTTTATATATCATTC         60040
Qy     839  ------------------------------------------------------------     839
Db   60039  CTTTTGTTTTTTCCTCAAACAAGGTTTCAGCAATTCTTATCCATTTTCTTCATATACTATGG  59980
Qy     839  ------------------------------------------------------------     839
Db   59979  AATGTTACAAATGGAGGTTTCTTTAAGTCCATTTTTAAATTAATGAGAATTTAAAACAAC   59920
Qy     839  ------------------------------------------------------------     839
Db   59919  CAACATCAAAATTGGGAGCAGAAATCCTGGTGTCTCCACGACAGTCCAGAAATCTAGTTCC   59860
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Qy     839  ------------------------------------------------------------     839
Db   59859  CTCCTACACACCCAAGTTATTCTTCAGAGAAGGGCCAAGTGTCTACCTGGTCTTCTCTGTCC   59800
Qy     839  ------------------------------------------------------------     839
Db   59799  CACAGTCCATTCTGCCAATCTGGGAAACAGAATGTGAAAACAGGAGAGTTTCTCTTTCAAGC   59740
Qy     839  ------------------------------------------------------------     839
Db   59739  CAACACAGTTCTCATGTCCGAAAAGCTATTCTAAACCAAAAAACTCTCTTCCAATTTGAAT   59680
Qy     839  ------------------------------------------------------------     839
Db   59679  CCCATGTAATTATGCATTCTCTTTATAAACTATATAAAATGTGGAGAAGTATTCATCACAT   59620
Qy     839  ------------------------------------------------------------     839
Db   59619  TTGAATTAAATGTCTTTTTACATTCACAGACGCCAATATGAGAAATGGCTTTATCTCATA    59560
Qy     839  ------------------------------------------------------------     839
Db   59559  AAGAATTTATAACCACATGCCATGTTACTTTCCTGTAATGTTCCTGAGTCCTTTTTAAGT   59500
Qy     839  ------------------------------------------------------------     839
Db   59499  TGCTATTTTTAAATTCTTTGCTAGAATAAAAATAATTATGTGATTACTTTATCTCTGCTATC  59440
Qy     839  ------------------------------------------------------------     839
Db   59439  TTTTTTTTTTTTTTTTTTTGAGACAGAGAAGTCTCACTCTGTTGCCCAAGCTGGA       59380
Qy     839  ------------------------------------------------------------     839
Db   59379  GTGCAGTGGGATGGATCTCAGCTCACTGCAACCTCCACCTCCCAGGTTCAAGTGATTCTCGT  59320
Qy     839  ------------------------------------------------------------     839
Db   59319  GCCTTAGCCTTCCTGAGTAGCTGGGATTACAGACATGTGCCACCATACCTGGTTAATTTTT   59260
Qy     839  ------------------------------------------------------------     839
Db   59259  GTATTTTTAGTAGAGACAGGGTTTTACCATGTTGGCCAGGCTGGTTTCGAACTCCTGGCC   59200
Qy     839  ------------------------------------------------------------     839
Db   59199  TCAAGTAATCGGCCCGCCTTGGCCTCCCAAAGTACTGGGATTACAATCATCATAAGCCATTGT  59140
Qy     839  ------------------------------------------------------------     839
Db   59139  GCCTAGCCATCTGCTATCTTTTACTTGAATGTTTCATAATTGTTAGGAGAGCTCCTTTGCA   59080
Qy     839  ------------------------------------------------------------     839
Db   59079  TGTGAACATAATGCTTACTAATGTTTTATTCTTCGTGTCTATGGAACAAGTTTAAATTGAA   59020
Qy     839  ------------------------------------------------------------     839
Db   59019  ATTCAGTATAAAACTTGAAATGGGGGTTAAACTTAGATCAGTAGTGACTAAATCTCAATAAGACA  58960
Qy     839  ------------------------------------------------------------     839
Db   58959  TTTTCCTTAAGCTTATCATCCAAAAGTGTCATTTTTTCTACTTATTTTCTGGGGAGGAAAG   58900
Qy     839  ------------------------------------------------------------     839
Db   58899  GAAGCTAAGAATATTTGTCAGGAAAAACTTACTGACTTGATATACTTAATATATGTCCCAGT   58840
Qy     839  ------------------------------------------------------------     839
Db   58839  GTGAGTGACTAGGAATTCACAAATGGGAAAAGATTAACCATTACTAATTTTTATTTCTATAT   58780
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Qy      840  ------------------------------------------------------------------  ---
Db    58779  TGTATTGTCCTGTTTATAAGAATAGCAACTGAGCCTTTGGAGAATATAACGTACTATAGTG  58720

Qy      854  ---------SerLeuThrArgGluLyseAlaPheGluGlnMetTyrGluMetLeuGlnThrGlnHis  873
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    58719  TCATTAACAAGGGAAAAAAGCCTTCGAGCAAATGTATGAAGAGATGCTTCAGACTCAACAC  58660

Qy      873  ------------------------------------------------------------------  873
Db    58659  AGGTGATTATAGATTCATACTGACTTCAAAAACTTAATTTTGTTCTGTAAAGGCAGTACT  58600

Qy      873  ------------------------------------------------------------------  873
Db    58599  CTCAAATGACTCCAGTGGTTGCCTGCTAATTCATTTGCTCTTTGAGCCTTTCCTAATAAT  58540

Qy      873  ------------------------------------------------------------------  873
Db    58539  GTCATGTGCATAATTTCTCATATGACTTCACCAAAGAGAAACTAGAAGAGGAAATTGAGGGCA  58480

Qy      902  eArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThrProGluGlyMetPheIle--  921
             ||||||||||||||||||||||||||||||||||||||||||::::
Db    58479  ACCACAATTAGAATAAAATATTTTAGGTCCTCTCACATTACCATTAACTGTCTCGTTACTAA  58420

Qy      873  ------------------------------------------------------------------  873
Db    58419  GTATGCACATTTTTCTTTATTTTCCTGAAAGAATATTAATGAAATAACATACGCAAGAAAG  58360

Qy      873  ------------------------------------------------------------------  873
Db    58359  AAAATAAAATTCGGGCAGGGGCGGCTGTGTCTCACACTGTAATCCCAGCCACTTTGGGAGG  58300

Qy      873  ------------------------------------------------------------------  873
Db    58299  CTGAGGTGGGCGGGATCACTTAAGGTCAACAGTTAGAGACCAGCCTGGCAAACATGATGAA  58240

Qy      873  ------------------------------------------------------------------  873
Db    58239  ACCCCATCTCTACTAAAAATGCAAAAAATTAGCTGGGTGGTGGTGCGCACACTTGTAGTCC  58180

Qy      873  ------------------------------------------------------------------  873
Db    58179  CAGCTACTTGGGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGCGGAGGTTGCAGTG  58120

Qy      873  ------------------------------------------------------------------  873
Db    58119  AGCTGAGATCATGCCATTACACTCCAACTCCAGCCTGACACAGCAAGAGAGAAAAGAG  58060

Qy      873  ------------------------------------------------------------------  873
Db    58059  CTCGGGCCCTTTACATTAAAATCCCTAAAAATAGTTTACATTTTAAATACGAATAATATACATA  58000

Qy      873  ------------------------------------------------------------------  873
Db    57999  ATAAATGCACTTACACTTTAATTTAAACTAGTCCTCCTTATCACATTGACTTAGTGAT  57940

Qy      873  ------------------------------------------------------------------  873
Db    57939  GCTTTTTATATTACTTTAACAGAAAGATAGCTTTTACTCTCTTTGGGACTCATACTTGTAG  57880

Qy      873  ------------------------------------------------------------------  873
Db    57879  TCGGCACACCCTTTAAATTCCCTATTCTGTTTAATGAAAGATTGTAATGGGACTTAGA  57820

Qy      873  ------------------------------------------------------------------  873
Db    57819  AAATCCTTCTAAATACCTAAACAAATCTTAACTCTTCACACTAGCCATCCTTTCACGGG  57760

Qy      873  ------------------------------------------------------------------  873
Db    57759  CTTTGCCCATTCATTTAACGTATATAAAGTTAAATTTGTTATACTGAACTAGAGAGTAT  57700

Qy      873  ------------------------------------------------------------------  873
Db    57699  ATGACTATAGGGAGAAAAGAGAATTAATAACATTAATCGTCTTTTCTCAAAGAATTCTCAGTAGT  57640

Qy      873  ------------------------------------------------------------------  873
Db    57639  AAAAAAAAAAAAATCACTTTCTCTTTCATCATTCGAAAAATGCCTTTCCACCAAATTATA  57580

Qy      873  ------------------------------------------------------------------  873
Db    57579  ACATTTCAAAGTCCTCTCTATTTATTACTCTACACATGTATTCAATTGACCTTGCTATAATT  57520

Qy      874  ----------ArgAsnThrSerLysGlyLysAlaGlnIleI  882
             ||||||||||||||||||||
Db    57519  CATGCCTCATTATTTGGTAAATTTGTACATTCCAGAAAATACCTCGAGAGAAAGCACAGAT  57460

Qy      882  eIleGlySerCysGlyThrAlaPheSerHisAlaPheIleTyrPheLeuAlaTyrAlaAlaGlyPh  902
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db    57459  TATTCGGAAGCTGTTATGCAATTCAGCCATGCCTTTATATATTTTGCCTATCGGCAGGGGTT  57400

Qy      902  eArgPheGlyAlaTyrLeuIleGlnAlaGlyArgMetThrProGluGlyMetPheIle--  921
             ||||||||||||||||||||||||||||||||||::::
Db    57399  TCGATTTGGAGCCTATTTAATTCAAGCTGGACGAATGACCCCAGAGGGCATGTTCATGTA  57340

Qy      921  ------------------------------------------------------------------  921
Db    57339  AGTCGTGGAAATAGTCCGGACCTGGTTAGCTCACACCTGTAAATTCCAACACTTTGAGAGGC  57280

Qy      921  ------------------------------------------------------------------  921
Db    57279  TGAGGCGGGTGGGATCACTTGAGGTCAGGAGTTTGAGATCAGCCTGACCAACATAATAAAA  57220

Qy      921  ------------------------------------------------------------------  921
Db    57219  CCCCATCTCTACTAAAAATACAAAAAATTAGCTGGGTGTGGTGGCGCGCCTCGTAATCCC  57160

Qy      921  ------------------------------------------------------------------  921
Db    57159  ACCTACTACTCAGGAGGCTGAGGCAGGAGAATCGATTGAACCCAGGAAATGGAGGCTGCAGTG  57100

Qy      921  ------------------------------------------------------------------  921
Db    57099  AGCTGAGATCACGCCACTGCACTCCAGCCTGGGCAACAAGAGTGAGACTCTGTCTCAAAAT  57040

Qy      921  ------------------------------------------------------------------  921
Db    57039  AAATAAATTAATTAATAAGTTGTGGAAATACATAAAACCTTGTAGGGGGTTCATGTACTTA  56980

Qy      921  ------------------------------------------------------------------  921
Db    56979  TTTACCAGAAAGAGTCTAGTTTTATATGAGTGTTATCATTTAAATCACATATGTGGAAAAG  56920

Qy      921  ------------------------------------------------------------------  921
Db    56919  GTATGCTTGAATTTTTTTAAGTTGGAATTTTAAATATACACATATTTTAAAATTTT  56860

Qy      921  ------------------------------------------------------------------  921
Db    56859  GTATTGATATATATATTAGTTACACATATTTTTGGATATTGGTATATATATTCA  56800

Qy      921  ------------------------------------------------------------------  921
Db    56799  TATGATGTTTAATGATCAAATCAGGGTAATTGGGATGAATTTTATTTTTAACAGAC  56740

Qy      921  ------------------------------------------------------------------  921
Db    56739  AATAATTGTACATTATTATATATTTTATGGGGTACAATGGGTTGTCTGATATATGTTAACA  56680

Qy      921  ------------------------------------------------------------------  921
Db    56679  CTGTGAAAATGATTAAATCGAGCTAAGTGTTTTGTTATTTAGTCTATAAGTACAGCAT  56620
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Db  56619 AACTGGTAAAATACTGATACTGATATAAGGCATAAAATCTGAATTAAATTCCCAGATGAA 56560
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Db  56559 TTGCTCTCTTGCTTCAGTTTACTGGAACATGGGAATGTGGGGGCAAAAATATGCCTTCTTGT 56500
Qy    921 ------------------------------------------------------------   921

Db  56499 CATTCATCCCTTAGGAAATTTGTGAGACATTATGAAACTCTCAGTGTGGGAGATGGCTTCC 56440
Qy    921 ------------------------------------------------------------   921

Db  56439 TAAAGTAAGACTGTACATCAGTGAGGATGAATTATTTGCTAAGCAAAATAATCCAGAAGAA 56380
Qy    921 ------------------------------------------------------------   921

Db  56379 ACACATATAAAATGAGTGGTTTCCCTTCAAAAATGTCACATTTGGAATTGAATGTGGTGTCC 56320
Qy    921 ------------------------------------------------------------   921

Db  56319 CAGTGAGGCTGCTTCTTCCCAAAGCATTAGGTTGGAGCTCCCTATTTGAAGTTCTGGTCA 56260
Qy    921 ------------------------------------------------------------   921

Db  56259 CATAATTATGAAATTTATTTGTTTTACCGGAAACACTCTAAATGCAACTGCTAAATTAGAAAAA 56200
Qy    921 ------------------------------------------------------------   921

Db  56199 TTAATTTGGAGTATTAAATTCTGAGCTGAGAGCCTAAAAATATCAGAAAGTTGCTAAATCCA 56140
Qy    921 ------------------------------------------------------------   921

Db  56139 TCATAAACGTCATTGCTAAGCCATTTAGAACTGGAGAAATCCATACAATACTTGACTCAAA 56080
Qy    921 ------------------------------------------------------------   921

Db  56079 AAAGTAACATTATGTTATTTTTTAACAAGCCACCAAAAAATGCACATCCAATGCGAAGTATC 56020
Qy    921 ------------------------------------------------------------   921

Db  56019 AGCCTCTTCACAATAATGAATTGGGAGATTACACCTGTTACAAGGAATGCTGCTATTTGGC 55960
Qy    921 ------------------------------------------------------------   921

Db  55959 AGAACACACTGGGCACTTCTCTTGGGGTTTTGTTTTCCCAAGTCTCAGGACATTACTTTGA 55900
Qy    921 ------------------------------------------------------------   921

Db  55899 ATATCCTTATTGTTGTTGGCATATTTGTATTTTCAGGATAGGTTCAATTTGAGAAATGGCCA 55840
Qy    921 ------------------------------------------------------------   921

Db  55839 AAAGACATTTAAAACCTAAGTAATTTCAGAATAACTTGGAATAATTTTTAGTTTCTATTCA 55780
Qy    921 ------------------------------------------------------------   921

Db  55779 CATGAAAATTTATTTATTTATTAAGCATTAAGTGAAGTCCCAGGAAGTTTCTTGTTAGG 55720
Qy    921 ------------------------------------------------------------   921

Db  55719 CACTGATAAGAAAACAGTCCAACCCAGTAGTTCACCAACCCAGTATTCCTAAATCTTACTTGACAC 55660
Qy    921 ------------------------------------------------------------   921

Db  55659 CAAAGCCACTTAGAAGTTTCCTGGAAGCACGAGATTTCCTTATAAAAATGGAATATATGGAAATGG 55600
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Db  55599 AATATCTGTATTTAAAAATTTCAACAGAAGGGGCTGGAGTGTGGCTTCATGCCTCTAATCC 55540
Qy    921 ------------------------------------------------------------   921

Db  55539 CAGCACTTTGGGAGTCCAGGCAGTGGGATCACCAAAGGTCAGGAGATTTCGAGACCAGCCT 55480
Qy    921 ------------------------------------------------------------   921


Qy    921 ------------------------------------------------------------   921
Db  55479 GGACAACCTGTGAAATGCTGTCTGTAGTCAAAAATACAAAAAATTAGCCATGTATGGCGGGTG 55420

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Db  55419 CATGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCATGAGAATCACTTGACCCGAGGAG 55360

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Db  55359 GCAGAGGTTGCAATGAGCCAAGATCACCACTGCACTCCAGCCTGGGATGACAGAGTGAG 55300

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Db  55299 ACTCTGCCTCAAAAAAATTTAAAAATAAAAATTCAACAGAAATTGCAAGTTCCCTGTCCTAT 55240

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Db  55239 GTTCTCCTAGCCTCTAAAAATAGTGTTGGTCACTATTGCCCATGTGAATTTATAAACCACAATT 55180

Qy    921 ------------------------------------------------------------   921
Db  55179 ATATTTAGGCTTGGGGTTTCATTCTGATTACATAAGACTAATTACTTAGGTAGATTAACAA 55120

Qy    921 ------------------------------------------------------------   921
Db  55119 GAAACAAAAATCTGAAATCACATAAATAATTAATTCAGCTCTCACCACCCCCGTGAGCCAGTTTTT 55060

Qy    921 ------------------------------------------------------------   921
Db  55059 CCTTTGTTCTAATATAATCCAGGCACTCCCAAGCTTGAAAGTTGGTTGTAATCCAAAAGT 55000

Qy    921 ------------------------------------------------------------   921
Db  54999 TTGTTTGCAAGCCAATAGTTTGAAACTCAAAAACATGTTTCCTCATGTTGCTCTAAACTT 54940

Qy    921 ------------------------------------------------------------   921
Db  54939 TCCACAGACTTCTTTAATCCCAGGGCGCCCGTTCCTTCTTCTGTATAACTAGTTTTGAGTATT 54880

Qy    921 ------------------------------------------------------------   921
Db  54879 AGTAGAAAGCAAGCCAATTAAACATATTCATTACTAAATGTACGAGAGTTTGATGATTTTCCA 54820

Qy    921 ------------------------------------------------------------   921
Db  54819 AATTCTCACAGAGAGAATTTCATCGTTTTCATCAATTTCTCGTCGACTACTCTTTCTTT 54760

Qy    921 ------------------------------------------------------------   921
Db  54759 GCTTTTGTAATCACACCTATAAAAAAAAATTAAGAGAGGCCAGGCCACACGGTGGCTCATGCCTGT 54700

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Db  54699 AGTCCCAACACTTTGGGAGGCCAGAGGTGGGGTGGATCACAAGGTCAGGAGAGTCAAGACTAG 54640

Qy    921 ------------------------------------------------------------   921
Db  54639 CCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAAATACAAAAATTAGCTGGGCATGG 54580

Qy    921 ------------------------------------------------------------   921
Db  54579 TGGTGGGCGCCTGTAATCCCATCTACTTGGGAGGTGAGGCAGGACAAGAAATTGCTTCAACCCC 54520

Qy    921 ------------------------------------------------------------   921
Db  54519 GGAGGTGGAGGTTGCAGTGAGCCGAGATCACACCACTGCACTCCAGCCTGGGCAACAGAG 54460

Qy    921 ------------------------------------------------------------   921
Db  54459 CAAGACTCCAACTCAGGAAAAAAAAAAAAAAAAATATATATATATATATACATATAAAATT 54400
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Qy    921  ------------------------------------------------------------  921
Db  54399  ACTGGATCCTGTTTTCAGCCAGGACTCTGTGTTGTTGGAGGGCTTAGAGCTCCCAGACC  54340

Qy    921  ------------------------------------------------------------  921
Db  54339  TTTCATCTATTACACTTTCATTGAGTTCTCATCCAATCTGTCAGTTTAAATACCACCT   54280

Qy    921  ------------------------------------------------------------  921
Db  54279  GTGTCCTGATAACTTCCTTCTGTATATTTCCAACTCTGACCCTGCCCTGAGCACAAGACC  54220

Qy    921  ------------------------------------------------------------  921
Db  54219  CTTATCCAATTACTTAGGAGACACCTCCACTTGGAGGACTAATATCTCAATGTGTTCAAA  54160

Qy    921  ------------------------------------------------------------  921
Db  54159  ACAGAATTAAGGTGTTTCTCCCCAAAGGTTATCTTCCCAGACTTTCCCATCCTTAACT   54100

Qy    921  ------------------------------------------------------------  921
Db  54099  AATAACACCAACCACCATCCACACAGTTGTCAGCCCAAAAATGTTGGGAGTCATCCCTGTT  54040

Qy    921  ------------------------------------------------------------  921
Db  54039  GCTTCTCTTGCCATTGTCCACCACATAAATCACTGATTCCTCATGACTCTAATTCCAAAA  53980

Qy    921  ------------------------------------------------------------  921
Db  53979  TTCTTCTCTCATCCTTCTTCACACTCATCCAAGCCCTCCCTGTCTTGACTGGGACCACTGCAA  53920

Qy    921  ------------------------------------------------------------  921
Db  53919  CAACCTCACCAATGTCCTTGGTGTGTCCCACTCCTTGCTTCCCTATAATCCATTCTTCCACACTGC  53860

Qy    921  ------------------------------------------------------------  921
Db  53859  AGCCAGACTGATCATTTAATGCACAAAATCCAATAGCACCAGTTTATTAAAAATTCTGCAAG  53800

Qy    921  ------------------------------------------------------------  921
Db  53799  ATCTAGATCTTCCCACTGAAATTTGAATAAAGGCCAAAGTCCTTACCATGACCTGAAAGAC  53740

Qy    921  ------------------------------------------------------------  921
Db  53739  CTTCATGATGGGGCTGCTGGCTTTCCAATTTCATCCACCTCTATCTCCCATGTTAA     53680

Qy    921  ------------------------------------------------------------  921
Db  53679  CTTACTCATCAGCCCCACACTTGCCATGTCTGTCCCTGGACCTCCCCATTGCACAGGGTCTTTC  53620

Qy    921  ------------------------------------------------------------  921
Db  53619  ACACTTGCTATTCTCTGCCTGGAATGGTCATTCCCAGGGCTTTGCTAAGCTACACTTTTT  53560

Qy    921  ------------------------------------------------------------  921
Db  53559  CTTACCACTCAGGCTTCCCCTGCTAAGTCCACTCCTCAGAGGGGACTTTCACCGATGGGTCC  53500

Qy    921  ------------------------------------------------------------  921
Db  53499  AAAGTAGTTCCCTTAACCCTCCCTCACACTCTCTTTCCCATCACCATATATTTGTTTT    53440

Qy    921  ------------------------------------------------------------  921
Db  53439  ACAACACTTATGACACTTTATGATCTATGAAATTATATATTTTGTTTTCCATATATTTATGAG  53380

Qy    921  ------------------------------------------------------------  921
Db  53379  TGCATAGACTGAGCACAAGTTGTAACCTATCTGTTCACTGATGTTTCCCAAAAGCCAAA   53320


Db  53319  AACAAGTGGGTGGGCACATAACAGACACACAATAAATATTATTAAAATGAATGACTGAATC  53260

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Db  53259  AAAATTAAGGGGGAGGAGGATTTGGAATGGTACATAATTAGGCAGAAGTACAGTCATTTCTGGAAAT  53200

Qy    921  ------------------------------------------------------------  921
Db  53199  GTGCCTTCCGGAGTCACCTTCACACTTTGAAAACAGGAGAGTCTGTTTTTTCACAAAATTTTTCT  53140

Qy    921  ------------------------------------------------------------  921
Db  53139  AATTTTCTTTCTTTTTCTACACCCATATGTCTAATAACCAGGTGCTTTGGGCAGGAGGACTGGA  53080

Qy    921  ------------------------------------------------------------  921
Db  53019  ACCTACTGAGATTTGTTTAGATTAAAGCTAAGAAAAAAATTTCTCAGTCGAAGAATGATAC  52960

Qy    921  ------------------------------------------------------------  921
Db  52959  AACCTCAAAATCATGCCAGTCACTTTCATCGCCTGCAAAATGAACACCCGTTAGGGATGTTTCC  52900

Qy    921  ------------------------------------------------------------  921
Db  52899  TTTAAGGGGGCTTTCCAAGACTGCCAAACCATTCCAATTACTTATGAAAAATTGCTATAAACCGGC  52840

Qy    921  ------------------------------------------------------------  921
Db  52779  TCTAAACTACCCTGTGAAATACTATGGTTCCCATTTACGATGAGAACAATTAAGACTC   52720

Qy    921  ------------------------------------------------------------  921
Db  52719  AAAGAGGTTACCTAACTTGCTCAAAGTTACATAATCGGTAAGTAGCGAGACGACAGATTCA  52660

Qy    921  ------------------------------------------------------------  921
Db  52659  AGTTCATGTTCCAGATTCCAGAGGTTTGGTTTACTCAACGTACATTATTATTATTATTA   52600

Qy    921  ------------------------------------------------------------  921
Db  52599  TTATTATTACAAAATTCGTGGCCAAACATTCATAGAATAATTTCTGTGAAATTATTTTTA  52540

Qy    921  ------------------------------------------------------------  921
Db  52479  TATAAATGGAACAGGTGACCTGCTAGTTGCTATTTTATAGCCCTAAAATATGAGAATGAA  52420

Qy    921  ------------------------------------------------------------  921
Db  52419  AAGTCCCAATATAAAAAATTTCTTCCCTGAGCTGGCTACCCATACTTCCTGAAATTTCTTTT  52360

Qy    921  ------------------------------------------------------------  921
Db  52359  AATTAAATTCATTAAAAAGGGGGTCTCTTCTTGAGATCATTTAAGGCATTTTAACTATATCAGAACA  52300

Qy    921  ------------------------------------------------------------  921
Db  52299  TATGAAGGACTGTTAACATAAGTAACAATTAAAGAATAGTACCACCTTGGTATTTCCC   52240

Qy    921  ------------------------------------------------------------  921
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Db  52239  AGTGCCCCAAGGGAGGAAGGAAAATAGAGAGCTATCTGAGCTAGAGCCACTGGTATCACTT  52180        Qy   921  ------------------------------------------------------------   921
Qy    921  ------------------------------------------------------------    921        Db 51099  ATTTCTACTATCCTAGAAGTTTATCTGAAATGAGCATTTAAAAATAAGGTGAATAAACATTTT  51040
Db  52179  TTCTTCTTCTTTTCTTTTCTTTTCTTTTTTTTTTTTAAGTTCTCGGCTCTGTCG         52120        Qy   921  ------------------------------------------------------------   921
Qy    921  ------------------------------------------------------------    921        Db 51039  CATTCTGCCACCTTACAGACAAGGCATAGGGCGTTTAGAGAAAATCTCTTGTTTAGGTTCT  50980
Db  52119  CCCATGCTGGAGTGGCACGAGTGCACGGATCTCAGCTCGGCCGCAAACTCCGGTTCCTGGATTCA  52060       Qy   921  ------------------------------------------------------------   921
Qy    921  ------------------------------------------------------------    921        Db 50979  CATGCACCCATGTGTAGTGTAAAACACTCACCTCTCCCTTTGTTAGTCCCTGGGTTAACACATTC  50920
Db  52059  AGCAATTCTCCCACCTCAGCCTCCTGAGTAGTTGGGACTACAGGCACATGTCACCACACC  52000        Qy   921  ------------------------------------------------------------   921
Qy    921  ------------------------------------------------------------    921        Db 50919  TATTTGTTTATTTCACTATATAAAATGTGTAGATTTAGAGTGTACAAAAATAAGTTTTATTTTATCC  50860
Db  51999  TGGCTAATTTCTGCATGTTTTTGGTGGGAGGACCAGATTTCACCATGTTGGGCCAGGCGGGTCT  51940        Qy   921  ------------------------------------------------------------   921
Qy    921  ------------------------------------------------------------    921        Db 50859  TATCTCTTTGTTGTTAGTCCCTTTCGGCTGGTTTCCAGCTGACTTGCCTTTTGCAATACCG  50800
Db  51939  CAAACTCCGGACCTCAAGTGATCCACCTCCCTTAGCCTCCCAAAGTGCTAGGATTACAGG  51880        Qy   921  ------------------------------------------------------------   921
Qy    921  ------------------------------------------------------------    921        Db 50799  ACCAAGAACCAATTCCTAATCAGGAGGAGGGTTTCGTGTAGCCTTCCCCACTGCAAAGC  50740
Db  51879  TGTAAGCCACCACACCAGCCTCAGTTTTGAGTTTCATCCAGTCAGAATACAGACAGAA  51820        Qy   921  ------------------------------------------------------------   921
Qy    921  ------------------------------------------------------------    921        Db 50739  TTTCCTCTATCTCTGTGGAGTTTCTTCCTATATTTTTCTATATCCAATATTATCAAGAAGCTAAGCA  50680
Db  51819  TAAGGGTACCCACACTTTTGGGAGTTAGGACAAAAGAGAGATTCTCTAGGGATTCCTCC  51760        Qy   921  ------------------------------------------------------------   921
Qy    921  ------------------------------------------------------------    921        Db 50679  GAGCAATAGGTAAGAAAGAATCAAGATATGGCAGCCCTCAAATACAGTAATAATAAAAGC  50620
Db  51759  AGTATTAAATGTGGTTATTGCCCAAAAGAGCCAACATAGCACTATGCATAAATGTCAAATAGA  51700        Qy   921  ------------------------------------------------------------   921
Qy    921  ------------------------------------------------------------    921        Db 50619  CACAGCTTTGAAAACTGCCTGAGAAGCAGAACCAGGCAGTTTATGGGGTGTGTTTCCTAGT  50560
Db  51699  TGAGATTTGTCTTCAACACCAAAAGAGGATTTGGGTCCTAGAGATCAAAATGTGGCCCCAACT  51640        Qy   921  ------------------------------------------------------------   921
Qy    921  ------------------------------------------------------------    921        Db 50559  TCTCTTAAAAACCAAAATGCAGTTTCTTGACAAGAAACCACACATTGTATTTCAAATAATAAATG  50500
Db  51639  ACCATGAATGTGTCACAAGCTCCCTTTAGACACACTCTAAAATGATACCTGGGCCTAGAAGACT  51580        Qy   921  ------------------------------------------------------------   921
Qy    921  ------------------------------------------------------------    921        Db 50499  TGATTATTGGCAAAAGAAGACAACATAGGGTGGTTTTTCAATGAGTATTAACAGTGGGTCGA  50440
Db  51579  CTGTACCTTCCAGAATCTAGGATGACAGAGACAGCTTCAATCTCATCGACTAGCTAAACCA  51520        Qy   921  ------------------------------------------------------------   921
Qy    921  ------------------------------------------------------------    921        Db 50439  TACCTTAACATAATAAAGGATGGACAGAAGGGAGCTAGGCCTGCACCATCATCTTTGCCC  50380
Db  51519  AAGAAAATTTACAAGAGAAAACTCCCTCCTACTAGAATTCTTCTTAGATAAAAAGACACTTTG  51460        Qy   921  ------------------------------------------------------------   921
Qy    921  ------------------------------------------------------------    921        Db 50379  TAGGAGGCTGGGGCTGGCCAGCCAGGGAAGAACTGTGAGTGTTATTGCTGTGGTTAAGGAAAGCAAC  50320
Db  51459  AGCCATTCTCTAAACCAATGGTTTTCCAACTCAGCAATCTAGGAGACTCGGTTAAAACTGTA  51400        Qy   921  ------------------------------------------------------------   921
Qy    921  ------------------------------------------------------------    921        Db 50319  ACTGGTTACAAAAACAGGAAAAACAGGAAAGACTTCTTTCCATGTTGGGCTGCCATGGCA  50260
Db  51399  GATACCTAGATCTCATCCTGCAAAATCTGATTGTTGAGATCTAGTATGGGGCAGGGAATCTT  51340        Qy   921  ------------------------------------------------------------   921
Qy    921  ------------------------------------------------------------    921        Db 50259  GCCACCTAGCTCTTGCCTGGCTCTCCCCAGAGATTATCCGGAAGAGACAGACAAGGACA  50200
Db  51339  CATTTTATCAAACATTCCAGATTACTCCAAGGCATAATTATTTATAGCTACAAGATCGGATTA  51280        Qy   921  ------------------------------------------------------------   921
Qy    921  ------------------------------------------------------------    921        Db 50199  AGATAAGAAGGCTAAATCACCACTGAAGGGACCTAAAGGAAGAGAGAAATCAAAGGACAGTT  50140
Db  51279  TCTGTGTCTCTTTCAAAAATGACANTTGTGTCTCAGAAAAGGGAGATACACACAAAGGGAGTTT  51220        Qy   921  ------------------------------------------------------------   921
Qy    921  ------------------------------------------------------------    921        Db 50139  GATATCTAGGGCCTTCAGGAAGGATTCTAAAATGGAAAGCAAGTGGGTAACAAACTCCAACAT  50080
Db  51219  TAACAGCAAAATTCTTTAAGTGCTCATAATATTAGTTTGTTGTCAGCAAGGCTTTTTTAGAGG  51160        Qy   921  ------------------------------------------------------------   921
Qy    921  ------------------------------------------------------------    921        Db 50079  GTAGGAAAAAGACCAATTCCAGCCAGCTTTCCACTGCAAGGAAGGAGACCCATGTAGGGGGAAAACA  50020
Db  51159  AAAAAGCCCTCTAAAAAGAAAAAAGACAACACGCATGTCTTATGGTGTAGAAGCCGTCTCT  51100
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Qy   921 --- 921

Db   50019 CAGAGAGGAAGGCAGCTCACGTTCCAAACCTACAAATCTCATGTCTTCTGGGCAAATTGCA 49960

Qy   921 --- 921

Db   49959 TAATTTTTTCTGAGCTAGAGACTCTCCTCATTCATTGACTGATAAGTTTCATTCTACTTATC 49900

Qy   921 --- 921

Db   49899 TCCTAGGTGATTAGATGGTGATCTTGTATGTATGAAAACATTCTATAAGATCCAAAGAAACCAA 49840

Qy   921 --- 921

Db   49779 GAGGTCTCTGGGTTGTATATGGATGAGCATGGGAAATAAATTTTTAATGACT 49720

Qy   921 --- 921

Db   49839 ATAAAGTTAGTTGCTTATTTCTCCTCCTATCTGTTGAGAAAGGATTTAGGGCGGGAA 49780

Qy   921 --- 921

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Qy   921 --- 921

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Qy   921 --- 921

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Qy   921 --- 921

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Qy   921 --- 921

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Qy   921 --- 921

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Qy   921 --- 921

Db   49359 AACTCCTGACCTCGTGATCCACCCACCTCGGCCTCCCAAAGTGCTGGAATTACAGGCATG 49300

Qy   921 --- 921

Db   49299 AACCACTCGCACACAGCTCCTGTTGAGTGACTTTAAAATATTTGTCATGATACCAAAATTACT 49240

Qy   921 --- 921

Db   49239 CCTCTTCATATATCCCAAAATGGGGTGAAACTCTCCAAGACCACAGTGACATGAGAGAATTG 49180

Qy   921 --- 921

Db   49119 AGATTTGAAGGATATGGTTAACTATGTTACGGAGTTATTCTACAATA 49060

Qy   921 --- 921

Db   49179 TTGGCCTGTACATTTCTCCCAGTTAGGTGTTCAGTTCAAATGCCTTCCAGAGCTTAAACC 49120

Qy   921 --- 921

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Qy   921 --- 921

Db   48999 AGGTAAGGACAAATTCTGTAGCAGAGACCAGTTTTTTTCCATGTGGTGGGCCCTTGGGCCTACCTT 48940

Qy   921 --- 921

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Qy   921 --- 921

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Qy   921 --- 921

Db   48819 GCAGTTCGAGACCAGCCTGGTCAACACAGAAAAATTAGCTAGGCATGGTGGTGCATGCCTGT 48760

Qy   921 --- 921

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Qy   921 --- 921

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Qy   921 --- 921

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Qy   921 --- 921

Db   48399 TACCTCCCACAAACAACAAGCTCTGAGTTGAAGGCCCTTCTCCCTTTCTCATTAATATTTC 48340

Qy   921 --- 921

Db   48339 CATTTTCAGAGGGACCTAACAAGGATGTCTGCCTCCTCAGACACATTTTTATTGTCTAAATGCTTACC 48280

Qy   921 --- 921

Db   48279 ATTACTGTTATAGTGGGAATGTTAGGACAGGTAGAGATTTTAGCATATATCCAAAATCATGG 48220

Qy   921 --- 921

Db   48219 GAAGAAGCTATTTCTCAGTTATGATTCAGAGAAGCCTCTACCCCTTTGGGACTAGAA 48160

Qy   921 --- 921

Db   48159 ACCAGGTCTCCTAACTCATATAATCCAATTATCTTCCAGTCACTGCCTGATTCTTGGATC 48100

Qy   921 --- 921

Db   48099 AGACTGAGGCTTAAGTCTGACAGTCCTGATTTTCCTTGCATTAAAAACACATTTAAAAAA 48040

Qy   921 --- 921

Db   48039 AAAAACCTTCTGATTTGGTTACCTAAACTCAGTGACCCATTTCTGAATGTTTATAGCTGGGT 47980

Qy   921 --- 921

Db   47979 ATCAAATAATTCAAAATGGCATTTTGAGCTTTAAAACACTTTCTGTAAAATATCAGTACTAAA 47920

Qy   921 --- 921

Db   47919 AAATGCCTTGACATCACTGAACTAAAATAACAAATTATTTTAGTGTGTTTATTTTTGTTTTTATA 47860

Qy   921 --- 921

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Db  47859 TTTTATACTGTGTTTGATCTTTGTAAAGCAACAGGATTCAGGATCTGAGGTCTAGGTCA 47800
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Db  47799 CTGAAGAGATTGCATCAGCATCTACCCTTTGATAGGCCCCATTGAGGGAGAAAT        47740
Qy    921 ------------------------------------------------------------   921

Db  47739 TCACAAGGAGCCCAGACGTGTTACTTTGCTGTTATCCAGCACTGCAAACAAGCAAACTGG   47680
Qy    921 ------------------------------------------------------------   921

Db  47679 GTTCTGTGATGACCCTTTACTGCTCTAAATGTTAAATATTGCCAGGGACACTGGTCCAGTT  47620
Qy    921 ------------------------------------------------------------   921

Db  47619 TTAGCCTGATTGTGCCGTTAGGGTTGGTTTGTTCATTCTAGTACAC                47560
Qy    921 ------------------------------------------------------------   921

Db  47559 TACTTTCATATCTAAAATGAAATCGAAAAATGAGAGGAAAATATTTAACCATGGTCAGGTC  47500
Qy    921 ------------------------------------------------------------   921

Db  47499 CTGTGCCACAGTCGAGTAAATATTCTGTGTGCTTCCAAACATCATTTGACACTTACCAT    47440
Qy    921 ------------------------------------------------------------   921

Db  47439 TTTATTAATTAACATGTTTTGAAACTGAGATCATAATCAATAACCTAAAAGGATCAAA     47380
Qy    921 ------------------------------------------------------------   921

Db  47379 GTTCTTCTTTCAGTCGTTTTTAGTCAGATTTTGCTTTGGGAACCTGAGGAAAATACGGATCC 47320
Qy    921 ------------------------------------------------------------   921

Db  47319 CCATGATTTGCTCTCCTAAATAAATGTAGCATATCAGACAGATAACCAGTCATTTAGCTTCA 47260
Qy    921 ------------------------------------------------------------   921

Db  47259 GTTATCTGTCCTACTACATTATATGCAAAACAAACAAAAAATCATATCTACTGTG        47200
Qy    921 ------------------------------------------------------------   921

Db  47199 TAAATCCAGATCTCACTACTGGGAGATTCATTCTTCCTATTGTCAGTGAATTCTCTGTCA   47140
Qy    921 ------------------------------------------------------------   921

Db  47139 AATCTCCAAGCAAGCAAGCCTCATATCAAGATGACTAAGAGAGTTTTATATTCACTAGTTG  47080
Qy    921 ------------------------------------------------------------   921

Db  47079 GGACCTTGATCTGTGGGCTCTAATTGGAAGAGACATTTTTAAGATTACCCAAGCTCCAAA   47020
Qy    921 ------------------------------------------------------------   921

Db  47019 GTTCATTTGGTGTACAGAGGCAAGGAATGATTACTACATGGTAGAAATTTTTAAAGAGA    46960
Qy    921 ------------------------------------------------------------   921

Db  46959 TAACTTGGTGGGTCTTCAGGGTTAGGGGTCCGGTCTACACCAAAAGATTATATTCCTGTG   46900
Qy    921 ------------------------------------------------------------   921

Db  46899 CCTGCTTTTTCTTTTACTTTTAGAGTTCTACTGTTTACAAAGGATCGATGGGACCTAAGA   46840
Qy    922 ------------------------------------------------------------   922
                   ValPheThrAlaIleAlaIleTyrGlyValAlaMetAlaIle              933

Db  46839 TTCAAATGCTTTATCTTTTGATAGAGTTTTTTACTGCAATTGCCATTATGGAGCTATGGCCAT 46780
Qy    922 ------------------------------------------------------------   922

Db  46779 CGGAGAAAACGCTCGTTTGGCTCCTGAAATATTCAAAAGCCAAATCGGGGGCTGGGCATCT   46720
Qy    933 ------------------------------------------------------------   953
          eGlyLysThrLeuValLeuAlaProGluTyrSerLysSerGlyAlaAlaHisLeu

Qy    953 uPheAlaLeuLeuGluLysGlyLysProAsnIleAspSerArgSerGlnGluGlyLysLysLysLeuLysSerPr 973
          |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  46719 GTTTGCCTTGTTTGGGAAAAGAAACCAAAATATAGACAGCCCGCAGTCAAGAAGAGGGAGAAAAGCC        46660
Qy    973 O-----------------------------------------------------------   973

Db  46659 AGTAAGCACAACTGTGTGATCTTAAAAATGTCCAAAATAAAGATGGCAACAGTAGGAACTGGGGG     46600
Qy    973 ------------------------------------------------------------   973

Db  46599 CCACTGAAGATGGGAGGAGGGGAGGGGCGCAAGGGCTGAAAACTAACCATTGGGGTGCTATA      46540
Qy    973 ------------------------------------------------------------   973

Db  46539 CTCAGTACCTGTGTGACAAGATCATTCATACCCCAAACATCAGCGATTATACCC             46480
Qy    973 ------------------------------------------------------------   973

Db  46479 AGACAACAAACCTGCCCATATACTCCTGGATCTAAAATAAAAATAAAAATGT               46420
Qy    973 ------------------------------------------------------------   973

Db  46419 AACATAAATGAAAAATAAAAATACCCACTTATTTATAAGAAGGCTGTCTT                 46360
Qy    973 ------------------------------------------------------------   973

Db  46359 TGGAAAACTCTGCAAAAGAAGATAATGTCATAGTAAACATAAAGAGAGTTAAAAGTTTGTGTCAAAA 46300
Qy    973 ------------------------------------------------------------   973

Db  46299 TAATTTATGGCTGCAAACGGGGAAAAAGGGGTCTTGTCTTAATCAAATTTTTACCTTCTAC      46240
Qy    973 ------------------------------------------------------------   973

Db  46239 AACTAAAATTTATATTTCATATTTTTAAAATATATATGCCTGATGCTA                   46180
Qy    973 ------------------------------------------------------------   973

Db  46179 TGAGAATGTTCTTTGAAAAAAAGAGATTGATTCTTATACTGAGAAACTAAAG               46120
Qy    973 ------------------------------------------------------------   973

Db  46119 TTTTGATCTTGGATGAAGATTCGTATTAAGGTTTATTGTTTCTTGATAATAT               46060
Qy    973 ------------------------------------------------------------   973

Db  46059 ATGCAAAGTAAATAATAATAATTCTGCTTCAGCACCATTTTTCATGGGAAATATATTTAC       46000
Qy    973 ------------------------------------------------------------   973

Db  45999 AAACAAAAGGGGGAAAAAAAGGAAAAGTATACCTTATTAAAATTGATGCACACAAACAAAATTTAG  45940
Qy    973 ------------------------------------------------------------   973

Db  45939 CCTCAAAACTCTAAAAGACTGTGAATATTAAAAGAGAAAATAATTAGGTAGGGTGTATAAATTT    45880
Qy    973 ------------------------------------------------------------   973

Db  45879 CAAAATAAATCTCAATAATAGTCTTATACAGCTCGGCGTGGCTCAGCCCTGTAAT            45820
Qy    973 ------------------------------------------------------------   973

Db  45819 CCCAGCACTTTGGGAGGCCCAGGTGGGTGGTGCAGGATCACGAGGTCATCCT               45760
Qy    973 ------------------------------------------------------------   973

Db  45759 GGCTAACATGGTGAAACCCCGTCTCTACTAAAAATAAAAAAAATTAAAAAAATTCAGCCGG      45700
Qy    973 ------------------------------------------------------------   973

Db  45699 GTGTGGTGGCGCACCGCACCTGTAGTCCCTACTCGGGAGGGCGGGAGGAGAGGAATCGCTT      45640
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Qy    973  ------------------------------------------------------------  973
Db  45639  GAACCCGGGAGGCGGAGGGTTGCAGTGAGCCGAGATCACGCCACTGCACTCCAGCCTGGGC  45580
Qy    973  ------------------------------------------------------------  973
Db  45579  GACAGACGAGACTTGCTCTCAAAAATAAATAAATAAATACAAAATAAATAGTAGTCTTA  45520
Qy    973  ------------------------------------------------------------  973
Db  45519  TACATTAAATATACATTCAATTTGTACTTTTCTAGACATTTTAATTTTTAAAATAAAA  45460
Qy    973  ------------------------------------------------------------  973
Db  45459  ATAGTCCATTAGGTATATACTTAAATGTTTTAACTTATATAATTATTCCCTCTAGAATTT  45400
Qy    973  ------------------------------------------------------------  973
Db  45399  TAATAGATTTATTATGTATGATGACAGCTTAAAATACGACATTACTACCAAATGGTTA  45340
Qy    973  ------------------------------------------------------------  973
Db  45339  AGAAGAATGCCTGTTAGTGACAGAAATAAGACTATCTCGGAAAATTCTCAAAAATGAAATGCT  45280
Qy    973  ------------------------------------------------------------  973
Db  45279  TCAAAGATACATCACAGTCAAAATAAGATTTTGTTCTTGTATTTTGGAAAGTAAAGGATG  45220
Qy    973  ------------------------------------------------------------  973
Db  45219  TAAGAGACTTTTTTTTTTAATTTTAAGATTATTATGTATGTAATACAGTAATTGCTACTCCCTATTTC  45160
Qy    973  ------------------------------------------------------------  973
Db  45159  TTTCTGCGAGATTATTAACAGAGGAATTGAGTATCTCACTGATCGTTAATAAATCTACGAACCA  45100
Qy    973  ------------------------------------------------------------  973
Db  45099  TAGGCATGGCATAGACTATGGAAGTGTTTCTTATAAAGGCTATAAAAATTAATGAATTTTAA  45040
Qy    973  ------------------------------------------------------------  973
Db  45039  TCCTTATTTATTTAGTATGTAAATGTTTCTGAATATCATCTTACGCTTTTAAAAAATTAA  44980
Qy    973  ------------------------------------------------------------  973
Db  44979  AATCTGGGCAGAGGGTGTGGTGGCTTACACCTGTAATCCCAGGACTTTGGGAGGCTGAGACG  44920
Qy    973  ------------------------------------------------------------  973
Db  44919  GGCGGATCACCTAAGGTCAGGAGTTCAGCCTGGTTAACATGGCAAAGCCCCATC  44860
Qy    973  ------------------------------------------------------------  973
Db  44859  GCTAACAAAAACACAAAAAATTAGGGTGTGGGGGCAAATGCCTGTCACCCCAGCTTGCTCGGG  44800
Qy    973  ------------------------------------------------------------  973
Db  44739  CACCACTGTACTCCAGCCTGGGTGACAGAGCGAGACTCCTTCTCAAAAAAAAAAAAA  44680
Qy    973  ------------------------------------------------------------  973
Db  44799  AGCCGAGGCAGGAGGATCGCCTTGAACCTGGGAGGCAGAGATTGCAGTGAGCCGAGATCA  44740
Qy    973  ------------------------------------------------------------  973
Db  44679  AATTAAAGTCTCGTCAAACAAAATTGGAAATTCCAGCTGGGTGATAGGTAT  44620
Qy    973  ------------------------------------------------------------  973
Db  44619  GTGGGCCATTTATTAAAATTTTCTCTATTTTTATACTTTTGGAGTTTTTCATATTAAA  44560
Qy    973  ------------------------------------------------------------  973
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Db  44559  TAGAATTAAAAAATCGTAAGAAATAAAATTTTAAAATGTTATTAAAATTTAGAAGTTTTCTAGAAT  44500
Qy    973  ------------------------------------------------------------  973
Db  44499  ACCTCTGTGAGCTATTATACAAAATACTTACGAAGAGCATACAAAAATAAATTGAATTCT  44440
Qy    973  ------------------------------------------------------------  973
Db  44439  TCATGTTTCTGCGGTATCTGTGTTTTTTTTAAAAACCTTTTTTTTTATACAAAATGCAGAGAGGGGA  44380
Qy    973  ------------------------------------------------------------  973
Db  44319  ATAGGTTGTAGGGGGGCAAATGGAAAATACTCACTACACTAAAAATAAAGACTACTACACT  44260
Qy    973  ------------------------------------------------------------  973
Db  44379  GTACCACAAAAAATTTTAAAAAATAAAACAAAAAGAAAAATTTTTTATACAAAATAATATTC  44320
Qy    973  ------------------------------------------------------------  973
Db  44259  ACTTTTAAATTTTGCAAAATATCCTTCCAGATTTTTTTTTCTATTTCTAGATCTCTTAA  44200
Qy    973  ------------------------------------------------------------  973
Db  44199  CCACATCTTAACATCAAATTCTTTTAACAAGAAAATAATATCATAAAAATTTTTTTGTTT  44140
Qy    973  ------------------------------------------------------------  973
Db  44139  ACTCCTCACCCTACCTGCCCTGCTTCTTACCCTATAATATGATGGGCTCAGAATGGGGTC  44080
Qy    973  ------------------------------------------------------------  973
Db  44079  AAACATGACTAGTAAACCTGACTGTAAGGATGTGTTTTAAAATCCAGCGACCATCACTACCAC  44020
Qy    973  ------------------------------------------------------------  973
Db  44019  CACACACATGCACACACACAATCCACTACTCCTTAGTTGTTTTAGTCTTAACAAC  43960
Qy    973  ------------------------------------------------------------  973
Db  43959  AAAAATTAATAAGACTTAAAATGCAATTGAGAGAGACACAAAGATCAAAAGAAACTTAAAA  43900
Qy    973  ------------------------------------------------------------  973
Db  43899  TCTTATGAACCAAATATATAAAGGGAAAGTTAATCATTTAGTGATTAGTTCTGGAAAGTCT  43840
Qy    973  ------------------------------------------------------------  973
Db  43839  TTTTTTAAACATCCTGGTGTAGAATGAGTATTGGTTTAGAAATCATTAACCAGTAAAGAGAT  43780
Qy    973  ------------------------------------------------------------  973
Db  43779  TGATCCACAGAGAGAAAAACTAAATGTTTAGGCAACTGTCACTGCCAAAATAATGGTCAAATTG  43720
Qy    973  ------------------------------------------------------------  973
Db  43719  AAAATAAAGATAGGGCTGGGTGTGGTGGCTCACGCCTGTAATCCCAGCACTTCGGGGAGGC  43660
Qy    973  ------------------------------------------------------------  973
Db  43659  CAAGGTGGGCGAGATTGCTTGAGTCCAGGAGTTTGGAACCAGCCTGGGCAACATAGTGAAA  43600
Qy    973  ------------------------------------------------------------  973
Db  43599  ACCCATCTCTACTAAAAATACAAAAAATTGGCTGGGCGTGGTGGCGCGCACGCTGTGGTCCC  43540
Qy    973  ------------------------------------------------------------  973
Db  43539  AGCTACTCAGGAGGCTGAGGTGGGGAGGATCGCTTGAGCCCGGGAGGTGGAAGTTGCAGTG  43480
Qy    973  ------------------------------------------------------------  973
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Db  43479  AGCCGAGATCACACCACTGCCTTCCAGCCTGGGGTGACAGAGCTAGACCCTTTCTCAAAATA  43420      Qy  1039  --------------------------------------------------------------  1039
Qy    973  --------------------------------------------------------------    973      Db  42339  CACCACTCATCCCACCTCCCAACTGTCAAAAACTTTATGCACGGGTTAAGGCTTATTGGAA   42280
Db  43419  AAATAAAATAAAATAAATAAAATAAGAAAGATAAATCAGAGAATTCAAAACATACTTCAC   43360      Qy  1039  --------------------------------------------------------------  1039
Qy    973  --------------------------------------------------------------    973      Db  42279  TCAGCTCCATGAAGTCATGCCTCTAATATCTAAAATAATGTAAATCTCCCATCCTTCGAA   42220
Db  43359  TATAAAACATGGCCCAATTTAGAGAAATAACCCTCATACATATAGTTTATGAGAACCCCA   43300      Qy  1039  --------------------------------------------------------------  1039
Qy    973  --------------------------------------------------------------    973      Db  42219  ACTAAGGATTGTTTTTCTTACCTGGCACTTGTCTTACTATACCTTATATTGTGGTTTTTC   42160
Db  43299  GCTCTTCTCGAATTAAGCAATAAAAGGTTTGTAAAGACAACAACCACATTAAAAAGAAAAACG 43240      Qy  1039  --------------------------------------------------------------  1039
Qy    973  --------------------------------------------------------------    973      Db  42159  CATTACCTTGTCCTCCCCCACCACCACCACCATCAGCACACACCCACACAAAGCTTCC     42100
Db  43239  TATTACCCAGATAAGCTGGTCAAACAACCAACTGCGGGAATGGAACTGTGTCTGTGCAGCAA 43180      Qy  1039  --------------------------------------------------------------  1039
Qy    973  --------------------------------------------------------------    973      Db  42099  TGTCCTTGCCTCCTGCCCGTACAAAAAGTTCCTAAAACTCAGACTGCCCATGTTAGTCCTC  42040
Db  43179  GCTGAAGGAGCAAGTGGTTTTTAGAAACTCAGTGAGTGAAGATAACAAGAA          43120      Qy  1039  --------------------------------------------------------------  1039
Qy    973  --------------------------------------------------------------    973      Db  42039  ATTCTCCTGCAACGTACAGTCTTTTCGCCCTTACAGATTCAATGAGTGTTTGCAAAAC    41980
Db  43119  ACACAGACACAAAAAATATAAACAAAAAGTGACAGAAACCCACTTGCAGTCAACAGCTCT   43060      Qy  1039  --------------------------------------------------------------  1039
Qy    973  --------------------------------------------------------------    973      Db  41979  AGAGTTTAGGGACTCAAAGGAGTCCTTGAAACTATGAGACACTCATCTA             41920
Db  43059  ACAGAGATGCATACATGTTTAAAATTAAAAGGCTCTGGAAAACATGCACAAATTTTCAAAA  43000      Qy  1039  --------------------------------------------------------------  1039
Qy    973  --------------------------------------------------------------    973      Db  41919  TTCGCACATAGCATAGCACACTCCCTCTTCTAAACCTTCCACAGTTAGGACATACCAGTC   41860
Db  42999  TGAACTGGGCCAGTATGCTACAGTGTGTTACAAACCTTCCCAAGTCATTCTTCTCAAACTCT 42940      Qy  1039  --------------------------------------------------------------  1039
Qy    974       ...AspThrCysGluGlyAsnLeuGluPheArgGluValValSerPhe            987      Db  41859  TATGCCATCAATCAGGTCCTTCATGCCCTGGCCCTCCCACTCCCAAGCTCCTCTCA      41800
Db  42939  GTCAAACTTCCTTTCACAGACACAGTGAAGGGAATTTAGAGTTCAGAAGTTCTCTTC     42880      Qy  1039  --------------------------------------------------------------  1039
                 |||  |||| |||  |||  |||  |||  |||  |||  |||  |||            Db  41799  TATCACTCCCCACGTCATCACTGTGCTTTTCTGTTTTTTTGGGGGCTTTTGTACG        41740
Db  42879  TTCTATCCAGTCGCCCAGGATGTTTCATCCTCCGTGGCTTATCCCTCCAGTATTGGAGCGA  42820      Qy  1039  --------------------------------------------------------------  1039
Qy    988  PheTyrProCysArgProAspValPheIleLeuArgGlyLeuSerIleLeuGlyArg     1007      Db  41739  TTTTTGTTTGTTTGTTGTTTTTTGAGACAGAGTCTTGCTCTGTCGCCCAGGCTGGAGTA    41680
Db  42819  GGAAAGACAGTAGCAATTGTGGGGAGCAGCGGCTGTGGGAAAGACACTTCTGTTTCAACTT  42760      Qy  1039  --------------------------------------------------------------  1039
Qy   1008  GlyLysThrValAlaPheValGlySerSerGlyCysGlyLysThrSerValGlnLeu     1027      Db  41679  CAGTGGCGTGAATCTCTGCTCACTGCAAACCCCGCCTCTAGGGTTCAGTCGGATTCTCATGC 41620
Db  42759  CTGCAGAGACTTTATGACCCCGTGCAAGACAAGTGGTAAGACAAGAACACACACT        42700      Qy  1039  --------------------------------------------------------------  1039
Qy   1028  LeuGlnArgLeuTyrAspProValGlnGlyGlnVal--------------            1039      Db  41619  CTCAGCCTCCCAAGTAGTAGCTGAGATTACAGGGCGTGTGCCACCAGTGTCCAGTTAGTTTT 41560
Db  42699  AATCTGGGGGGTTAGCAGTCCTTATTCTTAAACATTCACTACTAGGGCTTAAGCATCCCCACTGG 42640    Qy  1039  --------------------------------------------------------------  1039
Qy   1039  --------------------------------------------------------------  1039      Db  41559  TGTATTTTTTGTAGAAACGGGGTTTCACCAGTGTTAACCAGGGTTGTCTTGAAACTCCTAGC 41500
Db  42639  TTTGGGTGGGGCAAACAATGCGAGAGTTAAAAGAAAAAAATCTCTGTGTGACCCTTA      42580      Qy  1039  --------------------------------------------------------------  1039
Qy   1039  --------------------------------------------------------------  1039      Db  41499  CTCAAGTCATCTGCCCACCTCCCAGTCTCCTCATGTTCTTTAAACACACCTATG        41440
Db  42579  ACTAAGGACGAAGCAAACCATCACAAAAATGATGGTTAGGACTCTGAACTGAACCACAA    42520      Qy  1039  --------------------------------------------------------------  1039
Qy   1039  --------------------------------------------------------------  1039      Db  41439  AACCTTTCTTTTGCTATTGCCCTGACCAGAATGTCCCTTTGCCAGGCTCCTTCTTCTCACTGT 41380
Db  42519  AGGTCAAAGATTCTTCAACCATTCTGGCAGCAGAAATGTTGATCTTAGCCATGGAATTA    42460      Qy  1039  --------------------------------------------------------------  1039
Qy   1039  --------------------------------------------------------------  1039      Db  41379  TCAGTGCTTAGTCTGAAACGTCCTTCCTTAAGGCCTTCTTTGTACAACCCCTTCTCATGC   41320
Db  42459  CTTTAGAACAATGGGGTGCTGGAGATCTGGTCTAATGTTCACTCGTGGCTCCGTATTCTGT  42400      Qy  1039  --------------------------------------------------------------  1039
Qy   1039  --------------------------------------------------------------  1039      Db  41319  CTCTCCATACCCTCCCACTGCCTCAGTCGGCTACACCCTGTTACCCTGTCTTTAGGGTAC   41260
Db  42399  TGTGGTTTAAGACAGAGAGAACACACTGTCTCCCACCTCCTTAGTTCAGGCTTCTCGCTTTCC 42340
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Qy    1039  ----------------------------------------------------------  1039
Db   41259  TTTCCTTCCTCCTGAGTTTATTGTTCATGTGTTTATTGCATGCCTCTGCTA         41200
Qy    1039  ----------------------------------------------------------  1039
Db   41199  AAATATAAGCTACATCCATGGGGGGGGAGGGGGAGGGACAGCATTAGGAGGATATACCTAAT  41140
Qy    1039  ----------------------------------------------------------  1039
Db   41139  GCTAAACCATGAGTTAATGGGTGCAGCACACCAACACATGGTCACGTATACATATGTAACA  41080
Qy    1039  ----------------------------------------------------------  1039
Db   41079  AACCTGTAGTTGTTGCACAGTACCTAAAACTTAAAGTATAATAATAAAATTAAAA        41020
Qy    1039  ----------------------------------------------------------  1039
Db   41019  AAATATATATATATAAAGCTACAAAAGGGAAAAGAGAGCTTTCTCTTATTGACCCACTATTTCCC  40960
Qy    1039  ----------------------------------------------------------  1039
Db   40959  TGGTACTGGAAGAGTCCCCTCACGTAGTAGTCTCATCAAAATATGAGATGGTGTTG        40900
Qy    1039  ----------------------------------------------------------  1039
Db   40899  TTAAGAGTGTTGTTGTTATTTATTTATGTGAATAAACATGGCTGTGTGTGCAAGATGACACAGCT  40840
Qy    1039  ----------------------------------------------------------  1039
Db   40839  TTACATGTGGAGTACTGTATCACTCTCCACCTACTTTTTACTGGGCTTTCAGAAAAGTCAGG  40780
Qy    1039  ----------------------------------------------------------  1039
Db   40719  GATTTATGAGCCTTCCTTGGGTAACTTTATACTTTGAAATAGCTTGAAATTCCTATTCCTTC  40660
Qy    1039  ----------------------------------------------------------  1039
Db   40779  TCCTGTTTACAGTGGAGGGGGGGCAGTAGTGCAGTTACACGCTGTTTGCTTCTATACAACGTAT  40720
Qy    1039  ----------------------------------------------------------  1039
Db   40659  TTGTTTATGATTTGTGTGTTTGAATACAGTGTAACTGTAACATACAGTTGTGTGATC        40600
Qy    1040  ------LeuPheAspGlyValAspAlaLysGlu                            1048
            |||||||||||||||||||||||||||||||||
Db   40599  TTAACACCAATTCTCCAAATCTGCTTTGGCAGCTGTTTGATGGTGTTGGAAGCAAAGGAA    40540
Qy    1049  LeuAsnValGlnTrpLeuArgSerGlnIleAlaIleValProGlnGluProValLeuPhe  1068
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   40539  TTGAATGTACAGTGGCTCCGTTCCCAAATAGCAATCGTTCCTCAAGAGCCTGTGCTCTTC    40480
Qy    1069  AsnCysSerIleAlaGluAsnIleAlaTyrGlyAspAsnSerArgValValProLeuAsp  1088
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   40479  AACTGCAGCATTGCTGAGAACATCGCCTATGGTGACAACAGCCGTGTGGTGCCATTAGAT    40420
Qy    1089  GluIleLysGluLahAlaAsnAlaAsnIleHisSerPheIleGluGlyLeuProGlu    1108
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db   40419  GAGATCAAAGAAGCGCGAAAATGCAGCAAAAATATCCATTCTTTTATTGAAGGTCTCCCTGAG  40360
Qy    1108  ----------------------------------------------------------  1108
Db   40359  GTAAGAAAATTTCTGAAAATCTTGAATTATAAAGCTGCCAAGTAAGGCTAAGTAGCTACTG  40300
Qy    1108  ----------------------------------------------------------  1108
Db   40299  GGGCTATGCAGTGGTTTTTATGTATTACAAATGTATTATTTTATTGCCAGAATC         40240
Qy    1108  ----------------------------------------------------------  1108
Db   40239  TAAAGTTAGAGTATGTAAAACATGAACTCAGATGCGAAAAACCAAGTTTGAGATTTTCGTGTG   40180
Qy    1108  ----------------------------------------------------------  1108
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Db   40179  ACGATTTTCCTACGACACCAAAAATGTATTAATATTCACTGGATTAACTTTCACATTTTGTTA  40120
Qy    1108  ----------------------------------------------------------  1108
Db   40119  TTTGCCTTCCATCCATCTACACTGTGGCTGGTCCACACTATGACCTTCCCCGCCCACGGCGG  40060
Qy    1108  ----------------------------------------------------------  1108
Db   39999  AGAGGGATCTTTAAAAACAAAATTAGATCCTTATCCCTCCCCGTCTCACAACTGCCTCATG  39940
Qy    1108  ----------------------------------------------------------  1108
Db   40059  TAGCCTTCTTCATCTGCTGTTCCAGTCTTGCTCCTTTATCATTTTTCTTCCTCACACTAGTTAATC  40000
Qy    1108  ----------------------------------------------------------  1108
Db   39939  GCTCCCCTGTTGCGCTTAGGAATAAAAGCCCACACACCCCATGGGGAGGGGGGCTGCTGAAGGCCT  39880
Qy    1108  ----------------------------------------------------------  1108
Db   39879  CTGTAATCTGGGCCTGCTGTTTCCCAGCAACAACCTCACCACACAGTCGCTTTGCTGCA  39820
Qy    1108  ----------------------------------------------------------  1108
Db   39819  GCTGAGCTGGTCTCTCTCCGTGTCTCAAGAACATGCCAACTTGCTCCCACCTTAGGACATTT   39760
Qy    1108  ----------------------------------------------------------  1108
Db   39699  TAACTTTCTTTTTTTTTTTGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTTCCATG  39640
Qy    1108  ----------------------------------------------------------  1108
Db   39759  GCGTTTGCTGTTTCTCCAGCCTAGACCTCCCTTAGGTTGGGCATAGTAGTAGGGGCCT  39700
Qy    1108  ----------------------------------------------------------  1108
Db   39639  GTGCAATCTCAGCTCACTGCACTCCACCTCCCGGTGTTCAAGCAATTCTCCTGCCTCAGCC  39580
Qy    1108  ----------------------------------------------------------  1108
Db   39579  TCCCAAGTAGCTGGGATTACAGGCATGCCATCACGCGCCCGGCTAATTTTTGTAATTTTT  39520
Qy    1108  ----------------------------------------------------------  1108
Db   39519  AGTAGAGAAGGGGTTTCTCCATGTTGGGACAGGCTGGTCTCAAACTCCCGACCTCAGGTGA  39460
Qy    1108  ----------------------------------------------------------  1108
Db   39459  TCCACCGGCCTTGGGCCTCCCAAAGTGCTGGGATTACAGGGGTGAGCCATCGCGCCCGGCAA  39400
Qy    1108  ----------------------------------------------------------  1108
Db   39399  GTAGCACCTTAACTTTCAAGCCCTTTCAAATGTTACCTTTGCAGAGGCGTTTCCCTAAACA  39340
Qy    1108  ----------------------------------------------------------  1108
Db   39339  TCCTTATTTTTTAAAGTCCTCACCAGTCCTATCCCTATCACACTTTGTTCTTCAGGGCATGTA  39280
Qy    1108  ----------------------------------------------------------  1108
Db   39279  TCACAGTCTGAAAAAATTACCCTGAGCACTTAGTAGTTATTGTTAGTTGTTTCCCTTCCCCACT  39220
Qy    1108  ----------------------------------------------------------  1108
Db   39219  AGAGTGTAAGATCCTTTTTTATCACCTTGATGTCTGTAGTTGGGCGTGGGCAATTGGCACAA  39160
Qy    1108  ----------------------------------------------------------  1108
Db   39159  AATCTCAGAAAAGTCAAAAAATCTTGGCTAACTGTAGAGGAAGCCTTTGGTGTAGGTTGCAAGCAT  39100
Qy    1108  ----------------------------------------------------------  1108
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Db   39099 TGATACAAATCCAAAAAACAGTGCACAGAGAGGGATAATTGTAACTTTAAGTGTTTATAAT 39040
Qy    1108 ------------------------------------------------------------  1108
Db   39039 ATCTGAGTGTTTGCAACACACATACACACTAAAATAAATTAAATGAAATAAAAATAG     38980
Qy    1108 ------------------------------------------------------------  1108
Db   38979 AGATATTTTCATGTAGGGGCGGAATTCTACAGTGATTTTTATAAACTAAGTTTCTATCT   38920
Qy    1108 ------------------------------------------------------------  1108
Db   38919 CACTTTAAAGGAGGATAGTTAAATTTAACAAACCAATAATATACCAATAATATCTAGA    38860
Qy    1108 ------------------------------------------------------------  1108
Db   38859 GCCCTGTTCTTTGGTGAAGGCCAATAGCCATCATCATTCTTTATACTCTTTCCC        38800
Qy    1108 ------------------------------------------------------------  1108
Db   38799 TCACCAGCTCTTCTCCATACTACATAGTGCCTACACATGTACAAACAGGATTTCCCTTACTC 38740
Qy    1108 ------------------------------------------------------------  1108
Db   38739 TGGTAAGGGTTTGCAGTACTAAAGACATAGGAAGGATTCACATATTTTTATAAATATAG   38680
Qy    1108 ------------------------------------------------------------  1108
Db   38679 AGACACTGGTGAAGTGTCTTTTAATGGCAACTTCCTTTTTAACCATGACACTCACTGCATTG 38620
Qy    1108 ------------------------------------------------------------  1108
Db   38619 TTAATTGTGGTCAGATTGTTATCTGCATAATCTCGATAGTTGTTTATGTATTGTGAA     38560
Qy    1108 ------------------------------------------------------------  1108
Db   38559 ATGCTGCCCAAATTGATATATTTGTACCATTTAACTTTTATTCTTTTTCCTTTGAGACAAGGC 38500
Qy    1108 ------------------------------------------------------------  1108
Db   38499 CTCACTCTGTCACCAGGCTGGCAGTGGTGGTTCTCAGCCTCGAC                  38440
Qy    1108 ------------------------------------------------------------  1108
Db   38439 CTCCCAGGCTCACCTGAGTCTCCCGAATAGGTGGGGATCACAGGCACATGCCACCATGCCT 38380
Qy    1108 ------------------------------------------------------------  1108
Db   38379 GGCTAATTTTTGTATTTTTGTAGAGATGGGGTTTCATCAGTTGCTTAGGCTGGACTCA    38320
Qy    1108 ------------------------------------------------------------  1108
Db   38319 AGCTCCTGGGCTCAAGCAATTCACCCACCTCGGTCTCCCAAAGTTGCTGGAATTACAGGC  38260
Qy    1108 ------------------------------------------------------------  1108
Db   38259 ATAAGCCACCACATCTGGCCTAACTTTTTATTCTTAAATTGTTTATTATCTTTATTCTTT  38200
Qy    1108 ------------------------------------------------------------  1108
Db   38199 TTATTGTACCAGTGTCTCACATTTACTCAAAAATCACTGTGCTAA                 38140
Qy    1108 ------------------------------------------------------------  1108
Db   38139 CTTTTACAACAGACTTTGAAAACTAAGATGTTATTCCTTTAACATTTTTTCTAAAAGA    38080
Qy    1108 ------------------------------------------------------------  1108
Db   38079 CTAGCTTATTTTTCAGTGTTTTAAATTTTAACTTTAATTTACCTTCATGTCATTGTTCCC  38020
Qy    1108 ------------------------------------------------------------  1108
Db   38019 CCAAAAACACGTAGAAAAATAAGGAAAACCTGATACCAAAATAAAATAGTTTAAAAAAAT  37960

Qy    1108 ------------------------------------------------------------  1108
Db   37959 CAAATCAGATAAATTCCTAGAAAAAGCTTGCATATTACTAAAATGCCCTCGGTTAGTACCCTGG 37900
Qy    1108 ------------------------------------------------------------  1108
Db   37899 GGAGAATAAGGCTGCCCTCTTATGCTCAGTTGGCTGGGAAAAACGAAGAGAGGAAACCAG  37840
Qy    1108 ------------------------------------------------------------  1108
Db   37839 CCACGGCATTCCCAGCCCTTCTGGGAACCAAGAACTAAGCTAAATTCCACCATAGTACA   37780
Qy    1108 ------------------------------------------------------------  1108
Db   37779 GCAAGGATGCTGTAACTACCGGCATTTTACAGTATAAAGAAGTTCAATAACTTTCTTAAAGT 37720
Qy    1108 ------------------------------------------------------------  1108
Db   37719 TGTATAGAAACTCAGCATTTGAACCTGGATTCTTTGTGCTATCCTGAAGGGACGGAAAGG  37660
Qy    1108 ------------------------------------------------------------  1108
Db   37659 GTTCGTAACCATGGTGGTCCTTAGGGTTTCAGAGATGGGACAAAGGTGCCCTTGCTCCTC  37600
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Search completed: December 17, 2003, 15:16:53
Job time : 327 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 17, 2003, 14:29:55 ; Search time 85 Seconds
(without alignments)
2.289 Million cell updates/sec

Title:
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Searched: 1 seqs, 79611 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

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Scoring table: BLOSUM62

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	Ygapop	10.0	;	Ygapext	0.1
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	Delop	6.0	;	Delext	0.1

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Query Match	Length	DB	ID	Description
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ALIGNMENTS

RESULT 1
AC002486
LOCUS   AC002486   79611 bp   DNA   linear   PRI 22-AUG-1997
DEFINITION   Human BAC clone RG367O17 from 7p15-p21, complete sequence.
ACCESSION   AC002486
VERSION   AC002486.1   GI:2341014
KEYWORDS   HTG.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
    Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 79611)
  AUTHORS   Kalicki,J., Smith,A. and Gibson,A.
  TITLE   The sequence of H. sapiens BAC clone RG367O17
  JOURNAL   Unpublished (1997)
REFERENCE   2 (bases 1 to 79611)

  AUTHORS   Waterston,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (22-AUG-1997) Department of Genetics, Washington
    University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
  SUBMITTED By:
    Genome Sequencing Center
    Department of Genetics
    Washington University
    St. Louis MO 63108, USA
    http://genome.wustl.edu/gsc
    mailto:saplens@watson.wustl.edu

COMMENT
    NOTICE: This sequence may not represent the entire insert of this
    clone. It may be shorter because we only sequence overlapping
    clone sections once, or longer because we provide a small overlap
    between neighboring data submissions.

    This sequence was finished as follows unless otherwise noted:
    all regions were double stranded or sequenced with an alternate
    chemistry; an attempt was made to resolve all sequencing problems,
    such as compressions and repeats; all regions were covered by
    sequence from more than one subclone; and the assembly was
    confirmed by restriction digest.

    MAPPING INFORMATION:
    The sequence of this clone was established as part of a mapping and
    sequencing collaboration between the NHGRI Chromosome 7 Mapping
    Project (Eric D. Green, Director), John D. McPherson in the
    Department of Genetics (Washington University), and the Washington
    University Genome Sequencing Center. For additional information
    about the map position of this sequence, see
    http://www.nhgri.nih.gov/DIR/GTB/CHR7 or send
    mailto:egreen@nhgri.nih.gov

    SOURCE INFORMATION:
    This clone is from a release of the human BAC library. The library
    contains cloned DNA from human sperm. See: Shizuya et al., Proc.
    Natl. Acad. Sci. USA 89:8794-7 (1992); Kim et al., Genomics
    34:213-8 (1996). The clone is available from Research Genetics,
    Inc. (http://www.resgen.com).
    VECTOR: pBeloBAC11
    Selection: chloramphenicol

    NEIGHBORING SEQUENCE INFORMATION:
    The clone sequenced to the right is RG086D03. The actual start of
    this clone is at base position 1 of RG367O17. This clone is part of
    an unanchored island, orientation is unknown.

    This clone contains STS sWSS1805 (NID:g1113222).

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misc_feature    4733..4933      /note="similar to EST AA296743 (NID:g1949076)"
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repeat_region   6499..6859      /rpt_family="ALU"
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repeat_region   complement(10090..10285)   /rpt_family="L1"
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repeat_region   23345..23476    /rpt_family="ALU"
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us-09-873-409-5 (1-1222) x AC002486 (1-79611)

Alignment Scores:
Pred. No.:                0
Score:                    2587.29
Percent Similarity:       13.63%        Length:        79611
Best Local Similarity:    11.51%        Matches:       837
Query Match:              42.01%        Conservative:  154
                                        Mismatches:    209
DB:                       1             Indels:        6081
                                        Gaps:          28

Qy       1 MetIleLeuGlyIleLeuValLeuAlaSer------------LeuValAsnGlyAla------------  13
                                                          ||||            |||
Db   56460 ATAAATATTTGATTGTTTTCAGCTTTTTCTATATATTGTTACAAATGCTGCAAAGACCAGTTA  56519

Qy      14 -------------------Cys------LeuPro-----------LeuMetProLeuValLeuGly--  23
                             |||            |||        :::      ||||||||
Db   56520 TATAGATGAATCTTTGTATATATATTACCTTAGGGTGAAATTCCTTAAGTTGAATTTGGGGCT  56579

Qy      23 ----------------------------------------------------------------  23
Db   56580 GACTATGTATAGTTTTTTAAGCTTTTTTATCAAATGCTTTTGACTGCTATCATTATTTTTTTT  56639

Qy      23 ----------------------------------------------------------------  23
Db   56640 ACCCTCCAGTTCCACCTACAATTACCTTGATTGACTCCAATGGAACTTTTTCATATGAAAG  56699

Qy      24 ----------------------------Glu-----------MetSerAs  27
                                         |||         :::||||
Db   56700 TATTAAAAAATACTGAAAGAAGATATAAGTAGCAAGAAATGTTTTAAAAATACTAAATTTCTGA  56759

Qy      27 pAsn---------------------------LeuIleSerGly--------  32
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Db   56760 TAATAAGTGTAAAAGATACACTCTATGTTTTACCAGGAAACCTAGATCATTATATTCAATG 56819
Qy      33 ----------------------------------CyB----LeuVal--------------    35
Db   56820 CACTTCACTCTCATGGCATTGTTATTTTAGTTCTTTTTTCTTAGCATAAAATTTCCT     56879
Qy      36 GlnThrAsnThr------------------------------------------------    39
Db   56880 CAATCAAATAACTGTGATCGATTTTTATGTGTGTAACAAGATAAAAGTTGTGCTTCAG   56939
Qy      40 ----TyrSerPheArgLeuThrLeuThrTyrTyrValGlyIleGlyIleValAlaI     55
Db   56940 TCTCACATTCTAATACTCTTTCTTCAGTTGACCCTGTATTATGTTGGAATAGGTTGGC 56999
Qy      55 aAlaLeuIlePheGlyTyrIleGlnIleSerLeuTrpIleIleThrLeuArgGlnTh     75
Db   57000 TGCCTTGATTTTTGGTTTACATACAGAGTTTCCTTGTGGAATTATAACTGCAGCAGAC 57059
Qy      75 rIleAspArgIleArgLysGlyIlnPhePheHisSerValLeuValLeuAlaGIlnAspIleGlyTrpPheAs     95
Db   57060 CAAGAGGAATTCGAAAACAGTTTTTTCATTCAGTTTTGGCACAGACAGCACGGCCTGG 57119
Qy      95 pSerCysAspIleGlyLeuGluLeuAsnThrArgMetThr------------------    107
Db   57120 TAGCTGTGACATCGGGTGAACTTAACACTCGCATGACACAGAGTAAGGAGGATGATAT 57179
Qy     107 -----------------------------------------------------------    107
Db   57180 ACGTTAGCTTGTTTGTTTCATATGTAGACAATGAAATGACCTAACTACACATTATTTGCTTGTT 57239
Qy     108 -----AspIleAspLysIleAsnGlyIleIleGlyAspGlyIleGlyAsnLeuPheGlnA    126
Db   57240 TCAGTGACATTGACAAAATCAGTGATGGTAATTTGAGATAAGAGTTGCTCGTTTCAAA 57299
Qy     126 snMetSerThrPheSerIleGlyLeuAlaValGlyLeuValLysGlyTrpLysGlyThrI    146
Db   57300 ACATGTCTACTTTTTCGATTGGGCCGGCAGTTGGTTGGTAGGGCTGGAAACTCACC 57359
Qy     146 euValThrLeuSerThrSerProLeuIleMetAlaSerAlaAlaAlaCysSerArg---    164
Db   57360 TAGTGACTCTATCCACGTCTCCCTCTTATAAATGGCTTCAGCGGCGAGCATGTTCAGGGTAA 57419
Qy     164 -----------------------------------------------------------    164
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Qy     164 -----------------------------------------------------------    164

Qy     164 -----------------------------------------------------------    164
Db   57900 ACTGTGTCACACAGGGCTGGAGTGCAGTGGTGCAAAACATGGTTCACTGCGAGCCTCAAACTTC 57959
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Db   58800 TGTAAAGGAATAGAGAGTGGAGTAGTCTAAATTCTATTATATGTATTCATTGATCATCGGGAGAG 58859
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Db   58860 GAAGCAGGTGAAGGTCAGAGTTATCCAGTGAAGGTCGAGAGTTATCCAAAGGATGGGCGATAC 58919
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Qy    164 ------------------------------------------------------------ 164
Db  59160 TTTTTAGGTGGATAAGACTTGCTATGCGAATAGGCAATAGTGTATGAATTCACAGCTCTGAA 59219

Qy    164 ------------------------------------------------------------ 164
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Qy    164 ------------------------------------------------------------ 164
Db  59340 GTCACCAATAGTGATATATTTCCCTTTCTCTCTGAAATCTTACCTCTTAGTATTTGAGA 59399

Qy    164 ------------------------------------------------------------ 164
Db  59400 CAAATTTTTAAAAATACAGAGATAAAGTCTAAAAAAATACCATTAGTCTACTTAGAATTC 59459

Qy    165 ------------MetValIleSerLeuThrSerLysGluLeuSerAlaTyrSe 178
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Db  59460 AAAATTCTGCCTGACTAAAATGTTCAGAACATTAATACTACACAGAGTCATTTTTAACTG 59519

Qy    178 rLysAlaGlyValAlaValAlaGluGluValValLeuSerSerIleArgThrValIleAlaPheAr 198
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Db  59520 TGGTTGTGGGTTATTACAGATGGTCATTCTCATTGGACCAGTAAGGAATTAAGTGCCTATTC 59579

Qy    198 gAlaGlnGlyLysGluLeuGlnArgSerPheLeuLeuAsnIleThrArgTyrAlaTrpPh 218
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Qy    218 eTyrPheProGlnTrpLeuLeuSerCysValLeu***PheValArgTyrThrGlnAsnIle 238
           |||||||||||||||||||||||||||||||||||
Db  59640 GGCCCAGGAGAAGAACTTCAAAGGTCTTTCCTTTTAAAATAACAGAGATAGCTTGGTT 59699

Qy    238 uLeuAspAlaLysAspPheGlyIleLeuTyrGluAlaSerLysValSerLeuGlyVal 258
           |||||||||||||||||||||||||||||||||
Db  59700 TTATTTCCCAGTGGCTACTAAGTTGTGTTCTGTT-TTTGTAAGGTATACACAGAATCT 59758

Qy    258 aValTyrPhePheMetAsnGlyThrTyrGlyLeuAlaPheTrpTyrGlyThrSerLeuIl 278
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Db  59759 CAAAGATGCAAAAGGATTTTGGCATAAAAAGGACTATAAGCTTCAAAAGTGTCTCTTGGGTGC 59818

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Db  59819 TGTGTGACTTCTTTAGAATGGAAACCTATGGGTATGGACCTCCTTGAT 59878

Qy    292 --- 292
Db  59879 TCTTTAATGGAGAACCTGGATTACCATCGGGACTGTTCTTGCTGTAAGTCTTGTTTGAGA 59938

Qy    292 --- 292
Db  59939 ACAAGGTGTCAGGCCTGGATAAATCTTCCTTACCTTAGTTAGCCAAAAATTCCTCTTTGAA 59998

Qy    292 --- 292
Db  59999 GATAAATAATTCAAAAGATGGATGTTTTTATTAAAACAAATAATTGTTTCCCTTCAAATTATCT 60058


Db  60059 GTATACACCTTTAAATTATAAATTAGTTATGAATTGACAGCCATTTATTCATCCAGCATGTTTTAG 60118
Qy    292 --- 292

Db  60119 TGTCCTCGCTGTGTGTCAAGCATCCGCATTCCGCTTTGGAGGAATCATAATTGAATTCCCC 60178
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Db  60179 ACTGGGAAATACACTGAGTTTGTTGTTAATCTTAGCAGTGAAAAAGGGCCATTCTCTTGTGAGA 60238
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Db  60239 CTTTTCCTTTCATCTGGGCTGAGAATCAGAGACGGGAGTTCTGGCATTCACCTTGCTAAAAAGTCT 60298
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Db  60299 TCTCTCTGGAAATGGTCTGTAGAGTTTACACTCACCTCCTCTCCGTCCTTTCAGCA 60358
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Db  60359 TGTAGTAATTTAAAAAACGACTACATATAGCTCGTCCAGTAATACACAGTTTGGAGACTT 60418
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Db  60419 TTAAAATTCTTATGGGTTAGTGTTAAATAATAATTATTCAGTGTTATCCTCTTAAGTTACA 60478
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Db  60479 ATAAACAGATCAGTTCAGGATTAAGAAAACATTTGTCTTGAGGAACCAAAATGATCTGCTC 60538
Qy    292 --- 292

Db  60539 TTTTATACTTTGATCCTTGTTTGGCCTTTCCATTCTTACAGATTTCTCTCTTTCTTCCATTAA 60598
Qy    292 --- 292

Db  60599 ATTCATCTTTTTTGAATTTGAGGCATTCATAATTAAGACTTTTACTTATTTATTTCAT 60658
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Qy    292 --- 292

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Qy    292 --- 292

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Qy    292 --- 292

Db  60899 TCTGAGCCAATAAAAATCTACTGAATTTTCTTTTAAAGTTCAAGGGGTCACCCAACAG 60958
Qy    292 --- 292

Db  60959 GAGGGGAGTGCAACTCACCATGGGGTTTATACATGGTCAGCACACTTCAGTTAGCAGATT 61018
Qy    292 --- 292

Db  61019 TTTCTGGTCACAATCCCAGCATGTGATAACCACAAGACTATGAGATAATCAAAAGTTGT 61078
Qy    292 --- 292

Db  61079 TCCTTATTAGGAAAAAGGCCCAAGGATAACTTGGATTAATCTGTGTTTCTTATTGCTTCTCGGC 61138
Qy    292 --- 292
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Db  61139 CTTTTGGCTAAGATCAAGTGTAATCTGTGTTCTTTTTATTTGGTCANATCTTCCATTCT 61198     Qy    367 -------------------------------------------------------------- 367
Qy    292 ------------------------------------------------------------- 292     Db  62279 CGGCTAGTACTTTATCGCCTTTACACACGCACACACGCAGTTTATCGTGTACTCCA 62338
Db  61199 TTCTTACCTAATTCCTCTAAATATCTCTGTGAGCCTAAACCAATAATTATATATTACAT 61258     Qy    367 -------------------------------------------------------------- 367
Qy    293 ------------------------------------------------------------- 293     Db  62339 TCATTCAGTCTTTGACAAGTTCTTGTGAAAATGNGTGTCTCTTTTTATTGTGTCTTCCCCTT 62398
Db  61259 TCTATTGTCTTTCTTATATAATCTGCAGAAAGATAAATATCACTTGTTTGTTCCGTAGG 61318     Qy    367 -------------------------------------------------------------- 367
Qy    313 hrPheAlaIleAlaArgGlyAlaAlaPheHisIlePheGlnValIleAsp--------- 313     Db  62399 TCACTTCATTAGTGTATTTACCAAAAAAGTAGTTGTTGTTAAAGATTGCACAAGGCGATT 62458
Db  61319 TTTTTTTTTTAGTGTAATCCATAGCAGTGTTATTGCAATGGAGCAGCAGTCCCTCACTTTGAAA 61378     Qy    367 -------------------------------------------------------------- 367
Qy    293 alpPheSerVallleHisSerSerTyrCysIleGlyYAlaAlaValProHisePheGluT 313     Db  62459 ACTAATAAAACACTGGGCTTCATAGAAAAAGACATGATTTAAGTGAAAATAGATAAAATTA 62518
Db  61379 CCTTCGGCAATAGCCCGAGGAGCTGCCCTTTCATATTTTCCAGGTTATTTGATTAAGGTAAGAC 61438     Qy    367 -------------------------------------------------------------- 367
Qy    329 ------------------------------------------------------------- 329     Db  62519 CTAGTGTGATCAATTTCTAAGTCTGCCTACAGAATTGTTGTATAAAGACCTACCTACTCCTA 62578
Db  61439 CTCTTATTGCTTTGAAGAATAACTATCATTACTCTGCACAGAGGAGACAAAAAAACATACAC 61498     Qy    367 -------------------------------------------------------------- 367
Qy    329 ------------------------------------------------------------- 329     Db  62579 CTTCCTTATTTTTTTTCTGATTAAAAACTTTGATCGGAAAATTCTCTTTTCAAAGCTCTTTAG 62638
Db  61499 CCTCCATTTTCACTAAAACAAATAGGATGACAAATTTAAATGNTGGCCCAGTTGTTTATGGGA 61558     Qy    367 -------------------------------------------------------------- 367
Qy    329 ------------------------------------------------------------- 329     Db  62639 TTTTGAAAGTTGTTACTTAATTACCGATTACCAATTATTGGTATATAGTAATATGATTCCACCA 62698
Db  61559 AAGAGAGACTGCCTTAATTCTTTTCTCTAAGAGGAGGATTGGTGTTGTTGTATGATGAAAACCTTCATG 61618     Qy    367 -------------------------------------------------------------- 367
Qy    329 ------------------------------------------------------------- 329     Db  62699 TTTTTTCTTAACTGTACAGTATTTCAAAACTACCATTTTGCAACTGTATTTGGAITTGGCTTCC 62758
Db  61619 TCTAACTCAATGCACTTCTAAAGCAGAAAGGAAAACTGTCATGGAAGAAAACCATCCTTAT 61678     Qy    367 -------------------------------------------------------------- 367
Qy    347 IleGluGlyThrValGluPheLysAsnValSerPheAsnTyrProSerArgProSerIle 366     Db  62819 AACAACTATTTTAAAAATGAACTTTGTTAAACTAAGAATGA 62878
Db  61739 TGTTTTTTCCAAGAAACCCAGTATAGATAAACTTTTCCACAGCTGGATATAAACCTGAATCC 61798     Qy    367 -------------------------------------------------------------- 367
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Db    330 ------TGTTTTTTTCCAAGAAACCCAGTATAGATAAACTTTT 330     Qy    367 -------------------------------------------------------------- 367
Db  61679 ACTATTTTTAAAATGTAGAGACTNGTCAGTTTACTCCCTTTGAAGATTTATTAACATTCCTT 61738     Db  62759 TAGGGACTTCAGCACCAATGTGCCATTATATATTGCATGGGAAAGTGTTCTTTTGGGTTTTA 62818
Qy    329 ------------------------------------------------------------- 329     Qy    367 -------------------------------------------------------------- 367
Db  61859 AAGGTAGGTAATAAACAAATTACGCAATTGTGCAGTTTCTGATATTATCTTCTACTGGCC 61918     Db  62879 AATTTTGGGGGGGTCCACCTATTTTAAATAAATAAAATTCTTTCAGGAATGACCAGAAAC 62938
Qy    367 Lys- 367     Qy    367 -------------------------------------------------------------- 367
Db  61919 AAGATCTTCTCTGACATGATTACTTAGGATCACTTTTTTCCAAGATTTGGGCTACTTTGC 61978     Db  62999 CTCACCTCCTTCAGAGAACTTTCTCGGCTTGCCCTCGAAGGTTTTTATGTTTTGGCTTA 63058
Qy    367 -------------------------------------------------------------- 367     Qy    367 -------------------------------------------------------------- 367
Db  61979 TTAGAGACTTGAGGAGGTTAGATAAAATAATTAACTCTGGATCAACTAGTTATAT 62038     Db  63059 TGCAAAGGGTCCATTGCTTTACAAATGGTAGAATCAAAAGCAAGAGAGAATTCAAAGGGGAGAT 63118
Qy    367 -------------------------------------------------------------- 367     Qy    367 -------------------------------------------------------------- 367
Db  62039 TTTGCAGCATTCTTTCTATATTCAACTGACTAAAGCATTTTCAGCTCCGTGAAAATTCTTC 62098     Db  63119 TCCCCTGTTTAGGGCTAACTACTACATACGAGCAAGCAAAGATAGGTGAGAATTTCTCAAC 63178
Qy    367 -------------------------------------------------------------- 367     Qy    367 -------------------------------------------------------------- 367
Db  62099 TACTTCTGGGTTTGGGAACACACCTAAAATGTCTTGGGTTGACGCTGCCACCTGTTGGTGGT 62158     Db  63179 AGGATCACTGTTGTCAATTTCGAGAGGGGTAATTATTGTGAGGGCTTCAAATCACAATTGCAGGT 63238
Qy    367 -------------------------------------------------------------- 367     Qy    367 -------------------------------------------------------------- 367
Db  62159 TCCTAGATGCTACACCCACTCAACTACTCATTTTTAACCCCTCCTCTCTCTPAACCTTAGGGAGA 62218     Db  63239 CCCTGGCACACTAAAATGCTGTAGCAACCCCAGTCATTGAGAAAAATGTTTAAAGTGTTCCC 63298
Qy    367 -------------------------------------------------------------- 367     Qy    367 -------------------------------------------------------------- 367
Db  62219 ATTAATGCACATGNGCCTTTCCCTTCTTCCTGGGGCTTTTACTGCAGCAGCAATTG 62278     Db  63299 TCATGGGTCACCATGAGCCCACCAAGGGTTTCTAATGATAAACTCTCATCTATCGGGAGCC 63358
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Qy      367 ------------------------------------------------------------ 367
Db    63359 ACTAAGAAACTTTGCCAGCTGTTTTCCTTTAGAAATATGCTTTGCAAATTATGTTAGTATGT 63418

Qy      367 ------------------------------------------------------------ 367
Db    63419 CCTAAGGAGGAGCGCTTCATTAAATAGCTTGGTGTGAAAAATATCTGGCAAGATCTTCATTTACTTG 63478

Qy      367 ------------------------------------------------------------ 367
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Qy      367 ------------------------------------------------------------ 367
Db    63539 AAAATGTGACAGTTTTACTAGTTAATATTCTGAAGTACTCTTAATTAGTTAGTTCTCTTTACAT 63598

Qy      367 ------------------------------------------------------------ 367
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Qy      367 ------------------------------------------------------------ 367
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Qy      367 ------------------------------------------------------------ 367
Db    63719 GTTATAAATTAGTAGTACTCATTTTCTGAAAAGTGTCCATCACTCTCTTATGTGGGTTTTAT 63778

Qy      368 ------IleLeuLysGlyLeuAsnLeuArgIleLeuSerG 379
Db    63779 GATTTTCCCTCCAATACATTCCAATAGAATCTGAAAGGTCTGAATCTCAGAATTAAGTCTG 63838

Qy      379 lyGlnArgLeuTyrAspProAspAspGlyPhe- 399
Db    63839 GAGAGACAGTCGCCCTTGGTCGGTCTCAAATGGCAGTCGGGAAGAGTACGGTAGTCCAGCTTC 63898

Qy      399 euGlnArgLeuTyrAspProAspAspGlyPhe- 399
Db    63899 TGCAGAGGGTTATATGATCCGGATGATGGGCTTTGTAAGTGCAGCTAGCAAAACCATGCACA 63958

Qy      409 ------------------------------------------------------------ 409
Db    63959 GTCCACCTAATGGAATCTGGAAACACCGCAGGGCTGGGCACTCTTGTAACTTTTCATTTTTC 64018

Qy      409 ------------------------------------------------------------ 409
Db    64019 AACAGTAGGAGCTGGGAGAGAGGCCAATATTGTTTTCTTTCCTTTGTATCCATTCACTCAGC 64078

Qy      409 ------------------------------------------------------------ 409
Db    64079 AAAATATTTTATTTAGAGCCTACTATGTGTCAGGCACTCGTTTTAGGTTCTCGAGAATACCTTAG 64138

Qy      409 ------------------------------------------------------------ 409
Db    64139 GTGAATAAAACAGATAAAAATCTGCCTCATGAAGTTACATTCTAAATAATCAGAGGCAG 64198

Qy      409 ------------------------------------------------------------ 409
Db    64199 ACAATAAAAAATAAGTAAATTATATAGTATGTTAGAAGGGAGGGAATGTTGTGTGGAGAAA 64258

Qy      409 ------------------------------------------------------------ 409
Db    64259 AATAGCCGTATTAACATCTCGTACCAGTACTCAAAGAATTCAAAGTTTTGTTCCAGAAG 64318

Qy      409 ------------------------------------------------------------ 409
Db    64319 AATGATGTAGAAAAACATCTCCACTTTTCTTTTCCTTTTTTTTGGAGCTTACAG 64378

Qy      409 ------------------------------------------------------------ 409
Db    64379 TGTTGCACTTAACTTTCTCAGCCTTGTAAGTGGGCATAGAGGAATAAGACAGTGATTAATTCAA 64438
```

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Db    64439 AAGTGATTAATTCTTAATGCTTTCTGTTCGTTCAAACAGTTCAACACAGTTATTTTTTAAAAGAAATC 64498

Qy      409 ------------------------------------------------------------ 409
Db    64499 TACTCCCTAGAGCCTGGCTTTATTTAGTATTTTACTTCATAGTTTCATTTGGGTATCC 64558

Qy      409 ------------------------------------------------------------ 409
Db    64559 TAGACCCATGTGACTACATCATAAATTATTAGATGAGTGTATAAAAGAGTTGCATA 64618

Qy      409 ------------------------------------------------------------ 409
Db    64619 GAATATCCATCCCTGACAGAAAACAAGGGTTGGTTAAGAAAATAGAGACTCTATGAGTTAG 64678

Qy      409 ------------------------------------------------------------ 409
Db    64679 AATTACCAAACCTGGCTTCTGTCACGGGAATATGTGGGTAATTGGGACCAC 64738

Qy      409 ------------------------------------------------------------ 409
Db    64739 CCGTGGAGAAGCCAGAGGTCACTTATTATCATGAGAGTAGAGGACACTTTTG 64798

Qy      409 ------------------------------------------------------------ 409
Db    64799 TCTTTTGCAGAGGTGTGAGATGTTGAAATAATAGGCGGCTATTCCTAGAGAGAAATGTAAG 64858

Qy      409 ------------------------------------------------------------ 409
Db    64859 GGTCACATCCAAAAACTGAAGTTTTTTGTAGTGTCTACAATAATAACATTTGCGGAACCTA 64918

Qy      409 ------------------------------------------------------------ 409
Db    64919 GAGTATGTATCTTTATAAATACTAACTTGTGGATCTTAGAATAAAGATAATCAGATGATC 64978

Qy      409 ------------------------------------------------------------ 409
Db    64979 TGGCAAGGTTTTAGGCCAATATATTCTTTGCAGTTTGTTGGTGCCCATCTACCAGAAAA 65038

Qy      409 ------------------------------------------------------------ 409
Db    65039 AGTCTATGGACAATATATATGTTAGAAATATTTTATCAAAATATTATCAGTCTTTTGATTT 65098

Qy      409 ------------------------------------------------------------ 409
Db    65099 CTAAAATATGCTACTTCTCAGCTTATATTTGGTCTAGTATGAAAAAACCTAAAATCAAT 65158

Qy      410 ------IleMetValAspGluA 415
Db    65159 ACAGTAAAAGGCATCACAACATGGTTCATTCTTTCGGATTGGCAGATCATGGTGGATGAGA 65218

Qy      415 snAspIleArgAlaLeuAsnValArgHisTyrArgAspHisIleGlyValValSerGlnG 435
Db    65219 ATGACATCAGAGCTTTAAATGTCGGCCATTATCGGACCATATTGGGAGTGGTTAGTCAAG 65278

Qy      435 luProValLeuPheGlyThrThrIleSerAsnAsnIleLeuTyrGlyArgAspAspValT 455
Db    65279 AGCCCGTTCTTGTTCGGACACCATCAGTAACAATATCAACATTGGGACGAGATGAGTGA 65338

Qy      455 hrArgAspGluMetGluProPheIleMetGluP 475
Db    65339 CTGATGAAGAGATGGAGAGCCAGCAAGGGAAATGCCTATGATTTTATCATGGAGT 65398

Qy      475 heProAsn------------- 477
Db    65399 TTCCTAAATGTGAGTACACTGTGCACCCTGTGTCTTAGCTTATGTGTGGCAGCGCTGCGAC 65458

Qy      477 ---------------------------------------- 477
Db    65459 ATTCCAATATAAGGTAATGAAAACAACAACTGATGAGAATAGTAGGGGTGATTAAATT 65518

Qy      477 ---------------------------------------- 477
```

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Db  65519 CTGGATTGTCCTAGACAAGAAGCTTGTCCAACCAGTGGCACAAGATGGCTTTGAATGAGGTC 65578
Qy    477 ------------------------------------------------------------ 477

Db  65579 CAACACAAATTTGTAAAACTTTCTTAAACACATTATAATGAGATTTTTTGTGATTTTTAAATC 65638
Qy    478 ------------------------------------------------------------ 478

Db  65639 TTATCAGCTTATTGTTAATTTAGTGTATTTAAATGTGGCCCAAGACAATTCTTCTTTTCA 65698
Qy    480 ------------------------------------------------------------ 480
                                                          LysPheA  480

Db  65699 ATGTGGGCCCCAGGGAAGCCAAAAAAATTGGACACTCCTGTATGAAACATCTGTAGAGAAGAA 65758
Qy    490 et---SerGlyGlyGlnArgIleAlaIleAlaArg---------------LeuLysAs 502
                      ThrLeuValGlyGluLysGlyAlaGln-----M 490

Db  65759 TGCATAGTAACAACCAAAAGAGAAGAAATGCATCATTGAAAAGGCCAGAAAAAGAATCAT 65818
Qy    503 ------------AlaLeuValArgAsnProLysI 510

Db  65819 ATTTTGTTCTGCAATTGAAAAAGAAAAAAATGAAAAGATAAATGTTAAAGCATAACAAAGAA 65878
Qy    510 le------LeuIleLeuAspGluValThrSerAla 519

Db  65879 TATGAAAACAAAAATCATCA--GACCAAGCTGAGAAAAATTATGTCTAAAATGTTTATTTGGA 65936
Qy    520 -----LeuAspSerGluSer---------LysSerAlaValGln 529

Db  65937 GGCCATCTTGTGGCTGAGAGGTGGGAAGTCATACACAAGTTCAGATTGGTTCTGTGA 65996
Qy    529 ------------------------------------------------------------ 529

Db  65997 CAAACCACAAGAAAAAACTATGATCATTTTTTAAAGCACAGGAAGCTAACATTGCATAAGA 66056
Qy    529 ------------------------------------------------------------ 529

Db  66057 AATGTGAAATCAGGCCGCGGGTGCGGTGGCTCACCGGTGTAATCCCAGCACTGTGGGGAGGCC 66116
Qy    529 ------------------------------------------------------------ 529

Db  66117 GAGGTGGGCAGAATCACCTGAGGTTAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAA 66176
Qy    529 ------------------------------------------------------------ 529

Db  66177 TTCATCTTACTAAAAAGAACAAAAAATTAGCTGGGTGTGGTGGCGCACACCTTAGTCT 66236
Qy    530 -AlaAlaLeuGluLysLysLys------------Gly-ArgThrThrIleValV 544

Db  66237 CAGCTACTAGGGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGGAGAATTGCAGT 66296
Qy    544 alAlaHisArg 547

Db  66297 GAGCTGAGGATCGGCACCACTGCGCTCCAACCTGGACTGAGACTTTATGGGAAAA 66356
Qy    547 ------------------------------------------------------------ 547

Db  66357 AAAAGTGAAATCATATTTCGAAAGCAATATAGTCCCAAAAAGACTGAAAATCATATTTGGA 66416
Qy    547 ------------------------------------------------------------ 547

Db  66417 AAGCAATATAGTAAGCTAAAAATATTATTGTTAACCAGACTTACGAGGATCTTAATGGGTATTT 66476
Qy    548 ------Ser---ThrIleArgSer- 553

Db  66477 AGAATAATGGGGTGCTGTAAAGCCTTTTTTAAAAAATATTTCCTGAAGTATTAGAATCCT 66536
Qy    554 ---------AlaAspLeuIleValThr----- 559

Db  66537 CAGCATCCCCTGAAATTGTTGTTGGGGGGAGCACCTTGTTACATATGAAAGGATGAGAATTTGC 66596
Qy    559 ------------------------------------------------------------ 559

Db  66597 AATTAAAAATACAATATAAAATTCCACCATCCCAGAGAGGGTCACAATAACAGAAATGTTTATT 66656
Qy    559 ------------------------------------------------------------ 559
```

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Qy    559 ------------------------------------------------------------ 559
Db  66657 TTAATGGGGCATTATTTCACAAAACCAAAACTTGACGACGTGAATAATAATTTATTCTTCGGTTTT 66716

Qy    559 ------------------------------------------------------------ 559
Db  66717 TAATTTAAAAAATTTGTTATATGCCAGTAATTGTCTCTTGTCCCCATTATTTAGGATCATAA 66776

Qy    559 ------------------------------------------------------------ 559
Db  66777 TTAGGACATATTTAGGCCAAAAAAATCATTAAAGATTAAGGTGCTTCTTAAATCTTTGG 66836
                                                            LeuLysAs 562

Db  66837 GAACACACATTTCCTTTGTTGATGTTTTTGCCCCTTTCAATGACTTTCCTTAAAAC 66896
Qy    562 pGlyMetLeuUla---------GluLysGlyAla---------------His 572

Db  66897 ATCAATGCCTCCATTCCCACTTAGAATTAGGGAGACTTTCTGAATGCCTCTTAAAATCATAC 66956
Qy    572 a------GluLeuMetAlaLysArgGlyLeuTyrTyrSer- 583

Db  66957 CCTGTAAGTTACTTACTTGCTTTTACCAAAAAGGCCAAAAATACTACACAAAGATGTCCCTTGCT 67016
Qy    583 -----LeuValMetSerGlnAspIleLeuLysLysAla- 593

Db  67017 ATAAAATCTAATAATAAATCAGAAGATATTAACCAAAATAAATAAAATTAAAGATAGTAGCTTATC 67076
Qy    594 --AspGluGlnMetGluSerMetThrTyrSerThrGlu------ArgLysThrAsnSer 610

Db  67077 ATGATGAAAC-CTAAAATTCCACAGACCATAGCTAACCACAGAAAAAATGAGGAAACAACAATAAT 67135
Qy    610 ------------------------------------------------------------ 610

Db  67136 GAATGAAAAGTTCCAGAAGTGGCTAATTAGGTAGGTAAAAAATTGGGGAAAAGCTATTGTA 67195
Qy    610 ------------------------------------------------------------ 610

Db  67196 AAAAAAATGTATACATTACTTCCCTTATATAATATACACAGATTTTAAAATTAATGTATAAT 67255
Qy    611 ----LeuProLeu 613

Db  67256 AATTAGCTGATTACTGGTTAGCCTTTCACTCCATAAAACAACCATGAAAATTGGAATAAAACATA 67315
Qy    614 ----HisSer 617

Db  67316 TGAGGCCAAGGGCAGTCATTCCATGCATTGGATCAGAGAGTAAATCAAAAGACTGATTCCTA 67375
Qy    617 ------------------------------------------------------------ 617

Db  67376 ACAGAGAGGAAATCTCATAAAGGGTACTCCATGAATTCGTCGTGGGAACACTGAGCTGAAAG 67435
Qy    617 ------------------------------------------------------------ 617

Db  67436 GCAAAGCTCAAAATTTCAGGGGCAGCTTGGGCAGCTGGAAAGGTAGTAAGAAAATCACCTGTG 67495
Qy    617 ------------------------------------------------------------ 617

Db  67496 GCGATGAGGCAGGGGCAGAAGCCCAGTCTCTGTATGGGCATCCCTCAGGAAATCCTTGTCTGA 67555
Qy    618 -------------------------------------SerIleLysSer- 621

Db  67556 GGATAAGACTACCTACCCCAAGGCTCACCAGAGAGTGGCAGCCATAAAGCTGCAAGCGGGAA 67615
Qy    622 -----AspPheIleAspLysAlaGlu--GluSer 630

Db  67616 CACTGGGATAGAAGTCAGGCCGAGTGCTGCGGGGGGGGCGTTGAAAGTGCAGCGGTGGAAATGG 67675
Qy    630 ------------------------------------------------------------ 630

Db  67676 AGAGATCACATTAACACCTTTTTAACCCCCAGGGCAAGTAGTGCTAAAACACCAAAAAAGCC 67735
Qy    630 ------------------------------------------------------------ 630
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Qy       630 ------------------------------------------------------------ 630

Db     67736 ACACCTTAGGAGTCAGGACACACACCTTAGGAGTAAGATCTACCTGCCCTAACAAACCCTGA 67795

Qy       630 ------------------------------------------------------------ 630

Db     67796 GACCAAGCCATGACAGATGCCCAGAGGAGAGAGAGGTTTTGGGAGGTTGTGTTCTGCCAAGT 67855

Qy       631 ------------------------------------------------------------ 631
                                                                  ThrGlnSerL
Db     67856 TATGTGGCTTTTCTACAAATTCACCCCAAGCGAAACCTAAAATGAACAGTTCAA 67915

Qy       634 ysGluIleSer------------LeuPro--- 639
             :::   |||            |||||
Db     67916 GATCAGTCAGTTGCTTGAGTTGCCTACTAGAGACAAAAATCAGCACTGTTTTTTTTGTT 67975

Qy       640 -------------GluVal---Serleu------------LeuLys 646
                           |||:::      ||||||               :::
Db     67976 TTTGTTTTTGTTTTTCAGAAGAAAAACAGAACTTAGAGTCTCTTCAACCACAATTACAGT 68035

Qy       646 eLeuLys-----------LeuAsnLysProGlu----------TrpPro--- 655
             ||||              |||:::||||||            ||:
Db     68036 ACTCAGTACATCATTTACAAAAACCAGACATGCAAAGAAACAGAAAAATATGGCCTGTAT 68095

Qy       656 ------PheVal----------- 657
                   |||:::
Db     68096 GCAAGAAACATAATCCTAAAAGTTTATTCTTTAAGAAAAATACATGAAGC 68155

Qy       658 -------------Va 658
                           ||
Db     68156 AAAAACTGATACATCTGAAAGGAGAAAGACAAATCCACAACTTTAGTTGAGGCCTTCAGT 68215

Qy       658 -------------GlyThrLeuAla---------SerValLeuAsnGly--- 668
                           |||||||               :::::||||||
Db     68216 GCTTGATAGAACAAGCAGGTGGGATATCAGTAAGAATATAGATGAACAATACTAACAGGC 68275

Qy       669 -------------ThrValHisPro----------ValPheSer 675
                           |||                 ||||||
Db     68276 AGCTTAGATTTCACTGGCCATTTATACGACATTCCAGCCAACACAGCCAGAATACATTCTCA 68335

Qy       676 -------------IleIlePheAlaLysIleIleThrMetPhe----- 685
                           |||:::|||            |||:::|||
Db     68336 AGTGCACAGCCAAACATTCTCTAAAARTAAA--ACAATATTCTGGGCCATCAAAAACAAACAA 68393

Qy       686 -------------GlyAsnAsn--- 688
                           ||||||
Db     68394 ACAAAACTGTAGCCTCTTTCAAAATAATAAGAAAATATGTTCTCAGACCAATAAT 68453

Qy       689 -------------AspLysThrThrLeuLysHis--- 695
                           |||||||||           :::
Db     68454 ATAAGTAAACTACACAAATATTTGAAAAATCACAAAATAAACAATTCTAAAGAATATATATC 68513

Qy       696 --AspAlaGluIle----------TyrSer 701
               |||||                ||||
Db     68514 TCAAAAAGAAATTTCAAGAAAAATGAAAAACTATTCTGAACTAAATCAAAATGAAAATTG 68573

Qy       702 -------------MetIlePheVal--------IleLeuGlyVal-----IleCysP 712
                           |||||          |||||||         |||
Db     68574 CAAGTATTAGTAATTTGTGAGATATAGTTAAAGTATTTGCTCTGAGAGAAACTTAAGTAT 68633

Qy       712 heValSerTyrPhe-----------MetGlnGly-----LeuPhe---Ty 722
             ||:::||||||               :::|||      ||| 
Db     68634 TTAATGCTTATTTCGGAAAGAAAAAGAAAGATCTACAGTTCTGCAAACCTAATTTCACCTA 68693

Qy       722 r-----------GlyArgAla--- 725
                         ||||||
Db     68694 CAGAAAACTAGAGAGAGACGAAGCAAATTAACCCAAAACAACAGCAAGCTAGTAAATAGAAA 68753

Qy       725 ------------------------------------------------------------ 725

Db     68754 TTACAGTAGAAATCAGTAAAAACCAAAAAACTGAAAAAACATCAATTACTGAAAACCAAAAGCT 68813
```

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Db  69890 CCTTTACTTTACATCACACAAAAATTAATTTGCCATAGACCTTGTACCAAAATTGTAA 69949
                  |||
Qy    814 -AlaValThrGlyMetIleGluThr-------AlaAlaMetThrGlyPheAla------ 828
                  |||
Db  69950 AGCGTAAACTTCAAAAAATTAAAACTTACGAAAAAATCTTTGTAACTTTGAGAGGCAA 70009
                  ||| :::
Qy    829 ---------------------AsnLysAspLysGlnGlu------------------- 834
                  |||
Db  70010 AGTTTCTTAGACATGAAAAGCATTACTATAAAAAAGATAAAAACTGGAGTGTACTAAAGTT 70069
                  |||||||||
Qy    835 ----LeuLys-----His-------AlaGlyLysIleAlaThrGlu-A 845
                  |||| ||| |||||||
Db  70070 AAAAACCTCCTTTTTAAAACATCATTTAGAAAAACAAAAAAGGCAAG---ACAGAGAG 70123
                  ||||| :::||
Qy    845 laLeuGluAsnIle-----------------ArgThrIleVal------ IleGly- 853
                  |||
Db  70124 CACAGAAAAATATTTATTAATAATAACATGTCCGACAGACATGAAATCCAGAATATATAAAG 70183
                  ||||||
Qy    854 --SerLeuThrArgGlyLysAlaPheGlu----------GlnMetTyrGlu 866
                  |||||||||
Db  70184 AACTGCTATAGCTTGATGAGGAGACAAAATAGAATTAAAAATGGGCAAAAAATTTGAA 70243
                  ||||||
Qy    867 --GluMetLeuGln------ThrGlnHisArgAsnThr----- 876
                  :::||||||
Db  70244 CAGACATTTTACAAAAGAAGAATCAAATGAACAAATACATATAATTGAAAATATGACCATT 70303
                  ||||
Qy    876 -------------His-LeuPheAlaLeuLeuGluLysLysPro- 950
                  ||| :::||
Db  70304 ATTAGTCACCAGAGAGAACTCTAAATAAAAACGATAAATGAGGATACCATTTTACACTTCTAGA 70363
                  
Qy    876 ------------------------------------------A 962
                  
Db  70364 ATGGCCAAAATTAAAAAGACTAACAAAATGTAACTTTTGGTGATGATGAAGCAATATAGAT 70423
                  
Qy    877 -----SerLysLysAlaGlnIle---------IleGlySe 885
                  |||||||||
Db  70424 CTCTCATTCATTCAAAATAAAAAGTGAAAATCAGTATAAAATCACTAGAAAAGCAATTGGCAG 70483
                  |||
Qy    885 -Cys----------------TyrAlaPheS 890
                  |||
Db  70484 TTTATTATAATGTTAAACTATCAGACTCAGCCATTCTACCTAGGTATTTATTCA 70543
                  ||
Qy    890 er----------------------His---AlaPheI 894
                  ||| :::||
Db  70544 AAATAAATGAAAACATGACCACAAAAAATATCTCTACACATGAAATATTCAATAGCACGTTTTAT 70603
                  
Qy    894 eTyr-----------GluValSerPhe------ PheT 989
                  ||| :::||
Db  70604 TTATAATAGCCAAAAAATAGGAAACAAATTAAGTGTTCATCAGCAGTTGAATGAACAAATT 70663
                  ||||
Qy    896 ----------PheAlaTyrAlaAlaGlyPheGlyAlaTyrLeuIle--- LeuSerI 994
                  |||
Db  70664 GTGATAGAATCTAATTTTCCTTTTCCTTTTTTTTTTTTTGAATATGGG 70723
                  |||||||
Qy    909 ------------------------------------- 1017
                  
Db  70724 GTCTCACTCTGTCACCTAGGGTGAGTGCAAATGCACAATCTCAGCTCACTGCAGCCTCGA 70783
                  
Qy    909 -------------------------------------AlaPheVal---GlySerSer------ 1017
                  
Db  70784 CTTCCCAGGGCTCCAGGTCTTCCACCTTCCTGAGTAGCTTCATGCC 70843
                  ||||||
Qy    910 ----GlnAlaGlyArgMet--------ThrProGlu------ LeuSerI 917
                  |||
Db  70844 ACTACACCTGGCTAATTTTTGTATTTTTGTAGAGACAGGGTTTCACCATGTTGCCCAGG 70903
                  :::||||||
Qy    918 -------Gly--MetPheIleValPhe-----------IleGlyVal 1043
                  ||| ||| |||
Db  70904 CTGGTGTCAAACTCCTGGCTTCAACCAATCCACCACGTTGCTGGGA 70963
                  
Qy    923 ------------------------------------- 1053
                  
Db  70964 TTACAGGGTGTGAACCACCACGCCCGGACAAATTGTGATAGATCTTAGAGTTGCCAGATGAA 71023
                  
Qy    923 ------------------------------------- 1063
```

```
Qy   1064 -----------------------ProValLeuPheAsn----------------------------Cys 1070
                                    :::                                   |||
Db  72077 CAAATTTTCTTATGTCCTCTTCTTTCTTTGGGCCTCTTTTTTTTTTTTTTTTACGCGGGTTTGT 72136

Qy   1071 SerIleAlaGluAsnIleAla--------------------------------------------- 1077
                |||||
Db  72137 TTTCACAAAAGAACAAAATCAAAAAGACATAAGCACCCAGAGGCTGAGTACTGATTAAGCTG 72196

Qy   1078 -TyrGlyAspAsnSerArgValVal---------------------ProLeuAspGluIleLysGlu 1092
               ::| ::|  :: ||| :||                       ||||||||||||||||
Db  72197 ATATTAAAACACACTGGGAATTGTCAATTCCTGTTTCTAACCATTTGAT-------------- 72244

Qy   1093 AlaAlaAsnAlaAlaAsnIleHisSer------------PheIleGluGlyLeuProGlu--- 1108
                                                      ||||||  |||
Db  72245 --------------------------CACGCTGCCTTCGTTCTTCTGCTTCTTTCCTATTTTTC 72283

Qy   1109 -----LysTyrAsnThrGlnValGlyLeuLysValAlaGlnLeuSerGlyValGlyGlnLysG 1127
                |||||:||:| |||||||||||:|:|||||||||
Db  72284 ATTAGAAATTTAATACATTCGGTAGGGGGAAAAAAGGAGGTCAAATGAGTGGAGGAGAAAC 72343

Qy   1127 lnArgLeuValIleAlaArgAlaLeuLeuGlnLysProLysIleLeuLeuLeuLeuAspGlu 1147
             ||||||||:||:|||||||||:||||||||||||||||||||||||||||||||:|||||
Db  72344 AGAGGATCGGAATTGCTCGTCGCCTTAGTTCGAAACCCAAGATTCTGATTTTAGATGAGG 72403

Qy   1147 laThrSerAlaLeuAspAsnAspSerGluLysValGlnHisAlaLeuAspLysLysAla- 1166
             |||||||||||:::::||||||||||||:||||:|:::|
Db  72404 CTACGTCTGCCCTGGATTCAGAAAGGCAAGTCAGCTGTTCAAGCTGCCACTGGAAGGTAA 72463

Qy   1166 ---------------------------------------------------------- 1166
Db  72464 GTGAGCAGAGAAACGTTTCTTATTCATACTCCCTGGTTCATTATTGTTTTGAAGTACAAGA 72523

Qy   1167 -------------------------------------------------ArgThrGlyArgT 1171
                                                              |||||  ||
Db  72524 AAGTATAGATCTGTAATAGAATTACTTCAAGTTGAGAGCCCTTGAGGTATAAAGGCAGGA 72583

Qy   1171 hrCys------------------------------------ValThrHisArgLeuSerAla 1181
              :||||                                    ::: ||||::|
Db  72643 GATGCTGTGGTTGGTTGGGTGTGTAAAAATATATACACGAGGCTGATACACAGCAATCATCC 72702

Qy   1181 -------------------------------------------------LeuVal------- 1181
                                                               ||||||
Db  72584 TGTTAATCCACTGAGAACTTACGTGATGGCTATAGGAAGTGGTTTAGAGGACAGA-AGGA 72642

Qy   1181 ----------------------------------------------------- 1181
Db  72703 AGTCTATACCTCCATTCCAAGTGGTTTGCACTTTCCACCTCCCTAGAGGTGGCCCCACCACT 72762

Qy   1181 ----------------------------------------------------- 1181
Db  72763 ATCATCACTATTATTAACCATGCCCACCCTTTGCTTCTTCTTTCTTACATACACCTGTGGGATTCT 72822

Qy   1181 ----------------------------------------------------- 1181
Db  72823 CTTCCTCTGACCACTTTTTCTTCTTTAGGATACCCCCAGGTATTCATTTTGACCTAATTTCA 72882

Qy   1182 -----IleGlnAsn-AlaAspLeu---------------------------------- 1187
                 :||| ||| ||:||||||
Db  72883 CCTTCAAGTGGAGAATCGCTGAACCAGGCGCCCTTCGGACAGTCTCGGCCCCCTCAAA 72942

Qy   1188 -----eValValLeuHis------------------------------AsnGlyLysIleLys 1197
               :|||  |||||||                                ::::|||
Db  73003 TGTGGCCCTCGCACAAATTACACTGAATCTAGGAGGGGGAGTTGGCGGGTATGAAA 73062

Qy   1188 -----------------------------------------------------II 1188
                                                                  ::
Db  72943 CCTCACCCTGACCTCCTGCCTATGAGCTACTGCACATACCTCAAGGCCATATGCAGT 73002

Qy   1198 ------GluGln----------------------------------------- 1199
               |||||
Db  73063 AACCATTGAACAGTTTTCTCGAtGGGCCTGACTCCCTTATAAACCAGAGCCTTCAGACCCC 73122

Qy   1200 ------GlyThr-------------His------------GlnGluLeu-------- 1205
                                                      |||
Db                                    [bottom portion]
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```
Db  73123 TTACAAGGCTTAATGGCACATTTACTTTGCATTTGCATTTGGAAGTAGAGAGTTAAGCGTTTTT 73182
                                                ||||||                    ||||||
Qy   1206 ------LeuArg-AsnArgAspIle--TyrPheLysLeuVal---------AsnAlaGln 1219
                  ||||| |||||||:|||| ::: ||||||:::::                ::: |
Db  73183 TTTTCTCTAAGAAAAATCGCAGGCCTTCTCTTTTTTTAAAATGCTGACTTTATGGAAACCAGAAA 73242

Qy   1220 SerVal 1221
             :::
Db  73243 CGGATA 73248
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Search completed: December 17, 2003, 14:33:16
Job time : 200 secs